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=> file biosis caba caplus embase japio lifesci medline scisearch
=> e Norris steven j/au
E1            8     NORRIS STEVEN/AU
E2            3     NORRIS STEVEN H/AU
E3          239 --> NORRIS STEVEN J/AU
E4            1     NORRIS STEVEN J DR/AU
E5            1     NORRIS STEVEN JAMES/AU
E6            4     NORRIS STEVEN M/AU
E7            1     NORRIS STEVEN MARK/AU
E8            1     NORRIS STEVEN O/AU
E9            1     NORRIS STEVEN Q/AU
E10           3     NORRIS STEVEN R/AU
E11           1     NORRIS STEVEN RANDOLPH/AU
E12           3     NORRIS STUART/AU

=> s e3-e5 and borreli? and (VMP? or vls)
L1           47 ("NORRIS STEVEN J"/AU OR "NORRIS STEVEN J DR"/AU OR "NORRIS STEV
              EN JAMES"/AU) AND BORRELI? AND (VMP? OR VLS)
=> dup rem l1
PROCESSING COMPLETED FOR L1
L2           21 DUP REM L1 (26 DUPLICATES REMOVED)
=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 21 ANSWERS - CONTINUE? Y/(N):y

L2   ANSWER 1 OF 21  BIOSIS  COPYRIGHT (c) 2009 The Thomson Corporation  on STN
     DUPLICATE 1
AN   2009:232172  BIOSIS <<LOGINID::20090609>>
DN   PREV200900232172
TI   Detailed Analysis of Sequence Changes Occurring during vlsE Antigenic
     Variation in the Mouse Model of   ***Borrelia***   burgdorferi Infection.
AU   Coutte, Loic [Reprint Author]; Botkin, Douglas J.; Gao, Lihui;
       ***Norris, Steven J.***
CS   Inst Biol Lille, Lille, France
     Steven.J.Norris@uth.tmc.edu
SO   PLoS Pathogens, (FEB 2009) Vol. 5, No. 2, pp. Article No.: e1000293.
     http://www.plospathogens.org.
     ISSN: 1553-7366. E-ISSN: 1553-7374.
DT   Article
LA   English
ED   Entered STN: 1 Apr 2009
     Last Updated on STN: 1 Apr 2009
AB   Lyme disease   ***Borrelia***   can infect humans and animals for months
     to years, despite the presence of an active host immune response.  The
       ***vls***   antigenic variation system, which expresses the
     surface-exposed lipoprotein VlsE, plays a major role in B. burgdorferi
     immune evasion.  Gene conversion between   ***vls***   silent cassettes
     and the vlsE expression site occurs at high frequency during mammalian
     infection, resulting in sequence variation in the VlsE product.  In this
     study, we examined vlsE sequence variation in B. burgdorferi B31 during
     mouse infection by analyzing 1,399 clones isolated from bladder, heart,
     joint, ear, and skin tissues of mice infected for 4 to 365 days.  The
     median number of codon changes increased progressively in C3H/HeN mice
     from 4 to 28 days post infection, and no clones retained the parental vlsE
     sequence at 28 days.  In contrast, the decrease in the number of clones
     with the parental vlsE sequence and the increase in the number of sequence
     changes occurred more gradually in severe combined immunodeficiency (SCID)
     mice.  Clones containing a stop codon were isolated, indicating that
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continuous expression of full-length VlsE is not required for survival in vivo; also, these clones continued to undergo vlsE recombination. Analysis of clones with apparent single recombination events indicated that recombinations into vlsE are nonselective with regard to the silent cassette utilized, as well as the length and location of the recombination event. Sequence changes as small as one base pair were common. Fifteen percent of recovered vlsE variants contained "template-independent'' sequence changes, which clustered in the variable regions of vlsE. We hypothesize that the increased frequency and complexity of vlsE sequence changes observed in clones recovered from immunocompetent mice (as compared with SCID mice) is due to rapid clearance of relatively invariant clones by variable region-specific anti-VlsE antibody responses.

TI Detailed Analysis of Sequence Changes Occurring during vlsE Antigenic Variation in the Mouse Model of ***Borrelia*** burgdorferi Infection.

AU Coutte, Loic [Reprint Author]; Botkin, Douglas J.; Gao, Lihui; ***Norris, Steven J.***

AB Lyme disease ***Borrelia*** can infect humans and animals for months to years, despite the presence of an active host immune response. The ***vls*** antigenic variation system, which expresses the surface-exposed lipoprotein VlsE, plays a major role in B. burgdorferi immune evasion. Gene conversion between ***vls*** silent cassettes and the vlsE expression site occurs at high frequency during mammalian infection, resulting in sequence variation in the. . .

IT . . .
system; bladder: excretory system; ear: sensory system; joint: skeletal system; skin tissue: integumentary system

IT Diseases
Lyme disease: bacterial disease, ***Borrelia*** burgdorferi infection

IT Chemicals & Biochemicals
antibody

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi (species): pathogen, strain-B31

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 2 OF 21 MEDLINE on STN

AN 2006382551 MEDLINE <<LOGINID::20090609>>

DN PubMed ID: 16796669

TI Antigenic variation with a twist--the ***Borrelia*** story.

AU ***Norris Steven J***

CS Department of Pathology. University of Texas Medical School at Houston, PO Box 20708, Houston, TX 77225-0708, USA.. Steven.J.Norris@uth.tmc.edu

NC R01 AI37277 (United States NIAID NIH HHS)

SO Molecular microbiology, (2006 Jun) Vol. 60, No. 6, pp. 1319-22. Journal code: 8712028. ISSN: 0950-382X.

CY England: United Kingdom

DT Commentary
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)

LA English

FS Priority Journals
EM 200608
ED Entered STN: 27 Jun 2006
Last Updated on STN: 23 Aug 2006
Entered Medline: 22 Aug 2006
AB A common mechanism of immune evasion in pathogenic bacteria and protozoa is antigenic variation, in which genetic or epigenetic changes result in rapid, sequential shifts in a surface-exposed antigen. In this issue of Molecular Microbiology, Dai et al. provide the most complete description to date of the vlp/vsp antigenic variation system of the relapsing fever spirochaete, ***Borrelia*** hermsii. This elaborate, plasmid-encoded system involves an expression site that can acquire either variable large protein (vlp) or variable small protein (vsp) surface lipoprotein genes from 59 different archival copies. The archival vlp and vsp genes are arranged in clusters on at least five different plasmids. Gene conversion occurs through recombination events at upstream homology sequences (UHS) found in each gene copy, and at downstream homology sequences (DHS) found periodically among the vlp/vsp archival genes. Previous studies have shown that antigenic variation in relapsing fever ***Borrelia*** not only permits the evasion of host antibody responses, but can also result in changes in neurotropism and other pathogenic properties. The vlsE antigenic variation locus of Lyme disease spirochaetes, although similar in sequence to the relapsing fever vlp genes, has evolved a completely different antigenic variation mechanism involving segmental recombination from a contiguous array of ***vls*** silent cassettes. These two systems thus appear to represent divergence from a common precursor followed by functional convergence to create two distinct antigenic variation processes.
TI Antigenic variation with a twist--the ***Borrelia*** story.
AU ***Norris Steven J***
AB . . . et al. provide the most complete description to date of the vlp/vsp antigenic variation system of the relapsing fever spirochaete, ***Borrelia*** hermsii. This elaborate, plasmid-encoded system involves
an expression site that can acquire either variable large protein (vlp) or variable small. . . homology sequences (DHS) found periodically among the vlp/vsp archival genes. Previous studies have shown that antigenic variation in relapsing fever ***Borrelia*** not only permits the evasion of host antibody responses, but can also result in changes in neurotropism and other pathogenic. . . relapsing fever vlp genes, has evolved a completely different antigenic variation mechanism involving segmental recombination from a contiguous array of ***vls*** silent cassettes. These two systems thus appear to represent divergence from a common precursor followed by functional convergence to create. . .
CT *Antigenic Variation: GE, genetics
*Antigens, Bacterial: GE, genetics
*** Borrelia: GE, genetics***
****Borrelia: IM, immunology***

L2 ANSWER 3 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:87547 BIOSIS <<LOGINID::20090609>>
DN PREV200700093298
TI ***VMP*** -like sequences of pathogenic ***Borrelia*** .
AU Anonymous; ***Norris, Steven J.*** [Inventor]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]
CS Houston, TX USA

ASSIGNEE: Board of Regents The University of Texas System
PI US 07135176 20061114
SO Official Gazette of the United States Patent and Trademark Office Patents, (NOV 14 2006)
CODEN: OGUPE7. ISSN: 0098-1133.
DT Patent
LA English
ED Entered STN: 31 Jan 2007
Last Updated on STN: 31 Jan 2007
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
TI ***VMP*** -like sequences of pathogenic ***Borrelia*** .
AU Anonymous; ***Norris, Steven J.*** [Inventor]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George. . .
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
IT Major Concepts
Pharmacology; Clinical Immunology (Human Medicine, Medical Sciences); Infection
IT Chemicals & Biochemicals
Borrelia ***VMP*** -like DNA sequences: diagnostic-drug, immunostimulant-drug, immunologic-drug

L2 ANSWER 4 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 2
AN 2006:570967 BIOSIS <<LOGINID::20090609>>
DN PREV200600576492
TI Transcriptional regulation of the ***Borrelia*** burgdorferi antigenically variable VlsE surface protein.
AU Bykowski, Tomasz; Babb, Kelly; von Lackum, Kate; Riley, Sean P.; ***Norris, Steven J.*** ; Stevenson, Brian [Reprint Author]
CS Univ Kentucky, Coll Med, Dept Microbiol Mol Genet and Immunol, Albert B Chandler Med Ctr, MS 415, Lexington, KY 40536 USA
brian.stevenson@uky.edu
SO Journal of Bacteriology, (JUL 2006) Vol. 188, No. 13, pp. 4879-4889.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 1 Nov 2006
Last Updated on STN: 1 Nov 2006
AB The Lyme disease agent ***Borrelia*** burgdorferi can persistently infect humans and other animals despite host active immune responses. This is facilitated, in part, by the vis locus, a complex system consisting of the vlsE expression site and an adjacent set of 11 to 15 silent ***vls*** cassettes. Segments of nonexpressed cassettes recombine with the vlsE region during infection of mammalian hosts,

resulting in combinatorial antigenic variation of the VlSE outer surface protein. We now demonstrate that synthesis of VlsE is regulated during the natural mammal-tick infectious cycle, being activated in mammals but repressed during tick colonization. Examination of cultured B. burgdorferi cells indicated that the spirochete controls vlsE transcription levels in response to environmental cues. Analysis of PvlsE::gfp fusions in B. burgdorferi indicated that VlsE production is controlled at the level of transcriptional initiation, and regions of 5' DNA involved in the regulation were identified. Electrophoretic mobility shift assays detected qualitative and quantitative changes in patterns of protein-DNA complexes formed between the vlsE promoter and cytoplasmic proteins, suggesting the involvement of DNA-binding proteins in the regulation of vlsE, with at least one protein acting as a transcriptional activator.

TI Transcriptional regulation of the ***Borrelia*** burgdorferi antigenically variable VlsE surface protein.

AU Bykowski, Tomasz; Babb, Kelly; von Lackum, Kate; Riley, Sean P.; ***Norris, Steven J.*** ; Stevenson, Brian [Reprint Author]

AB The Lyme disease agent ***Borrelia*** burgdorferi can persistently infect humans and other animals despite host active immune responses. This is facilitated, in part, by the. . . vis locus, a complex system consisting of the vlsE expression site and an adjacent set of 11 to 15 silent ***vls*** cassettes. Segments of nonexpressed cassettes recombine with the vlsE region during infection of mammalian hosts, resulting in combinatorial antigenic variation. . .

ORGN . . .

Notes

Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier

Spirochaetaceae 06112

Super Taxa

Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name

Borrelia burgdorferi (species): pathogen

Taxa Notes

Bacteria, Eubacteria, Microorganisms

GEN ***Borrelia*** burgdorferi vlsE gene (Spirochaetaceae): expression

L2 ANSWER 5 OF 21 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 3

AN 2006:664489 CAPLUS <<LOGINID::20090609>>

DN 145:183820

TI Antigenic variation with a twist: The ***Borrelia*** story

AU ***Norris, Steven J.***

CS Departments of Pathology & Laboratory Medicine and Microbiology & Molecular Genetics, University of Texas Medical School at Houston, Houston, TX, 77225-0708, USA

SO Molecular Microbiology (2006), 60(6), 1319-1322
CODEN: MOMIEE; ISSN: 0950-382X

PB Blackwell Publishing Ltd.

DT Journal; General Review

LA English

AB A review. A common mechanism of immune evasion in pathogenic bacteria and protozoa is antigenic variation, in which genetic or epigenetic changes result in rapid, sequential shifts in a surface-exposed antigen. Dai et al. provide the most complete description to date of the vlp/vsp antigenic variation system of the relapsing fever spirochaete, ***Borrelia*** hermsii. This elaborate, plasmid-encoded system involves an expression

site that can acquire either variable large protein (vlp) or variable small protein (vsp) surface lipoprotein genes from 59 different archival copies. The archival vlp and vsp genes are arranged in clusters on at least five different plasmids. Gene conversion occurs through recombination events at upstream homol. sequences (UHS) found in each gene copy, and at downstream homol. sequences (DHS) found periodically among the vlp/vsp archival genes. Previous studies have shown that antigenic variation in relapsing fever ***Borrelia*** not only permits the evasion of host antibody responses, but can also result in changes in neurotropism and other pathogenic properties. The vlsE antigenic variation locus of Lyme disease spirochaetes, although similar in sequence to the relapsing fever vlp genes, has evolved a completely different antigenic variation mechanism involving segmental recombination from a contiguous array of ***vls*** silent cassettes. These two systems thus appear to represent divergence from a common precursor followed by functional convergence to create two distinct antigenic variation processes.

RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Antigenic variation with a twist: The ***Borrelia*** story

AU ***Norris, Steven J.***

AB . . . et al. provide the most complete description to date of the vlp/vsp antigenic variation system of the relapsing fever spirochaete, ***Borrelia*** hermsii. This elaborate, plasmid-encoded system involves
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ST review antigen ***Borrelia***

IT ***Borrelia***
(antigenic variation in ***Borrelia***)

IT Antigens
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(antigenic variation in ***Borrelia***)

L2 ANSWER 6 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2006:134820 BIOSIS <<LOGINID::20090609>>

DN PREV200600145254

TI ***Vmp*** -like sequences of pathogenic ***Borrelia*** .

AU ***Norris, Steven J.*** [Inventor]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]

CS Houston, TX USA
ASSIGNEE: Board of Regents, The University of Texas System

PI US 06878816 20050412

SO Official Gazette of the United States Patent and Trademark Office Patents, (APR 12 2005)
CODEN: OGUPE7. ISSN: 0098-1133.

DT Patent

LA English

ED Entered STN: 22 Feb 2006
Last Updated on STN: 22 Feb 2006
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
TI ***Vmp*** -like sequences of pathogenic ***Borrelia*** .
AU ***Norris, Steven J.*** [Inventor]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George. . .
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
IT . . .
Clinical Immunology (Human Medicine, Medical Sciences); Infection; Clinical Chemistry (Allied Medical Sciences); Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Diseases
Borrelia infection: bacterial disease, drug therapy, prevention and control
IT Chemicals & Biochemicals
DNA sequences; ***Vmp*** -like sequences; ***Borrelia*** polypeptide antigens: diagnostic-drug, immunostimulant-drug, immunologic-drug
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia (genus): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 7 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2004:283015 BIOSIS <<LOGINID::20090609>>
DN PREV200400283530
TI ***VMP*** -like sequences of pathogenic ***borrelia*** .
AU ***Norris, Steven J.*** [Inventor, Reprint Author]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]
CS ASSIGNEE: Board of Regents, The University of Texas System
PI US 6740744 20040525
SO Official Gazette of the United States Patent and Trademark Office Patents, (May 25 2004) Vol. 1282, No. 4.
http://www.uspto.gov/web/menu/patdata.html. e-file.
ISSN: 0098-1133 (ISSN print).
DT Patent
LA English
ED Entered STN: 9 Jun 2004
Last Updated on STN: 9 Jun 2004

AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
TI ***VMP*** -like sequences of pathogenic ***borrelia*** .
AU ***Norris, Steven J.*** [Inventor, Reprint Author]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor];. . .
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
IT Major Concepts
Equipment Apparatus Devices and Instrumentation; Infection; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Diseases
Borrelia infection: bacterial disease
Borrelia Infections (MeSH)
IT Diseases
Lyme disease: bacterial disease, diagnosis
Lyme Disease (MeSH)
IT Diseases
relapsing fever: bacterial disease, diagnosis
Relapsing Fever (MeSH)
IT Chemicals & Biochemicals
Vmp -like polypeptides: encoding DNA sequences, encoding amino
acid sequences; antibodies
IT Methods & Equipment
Borrelia infection assay method: bioassay techniques, laboratory techniques; immunodiagnosis: immunologic techniques, laboratory techniques; immunoprophylaxis: immunologic techniques, laboratory techniques; immunotherapy: clinical techniques,. . .
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia (genus): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 8 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2004:257493 BIOSIS <<LOGINID::20090609>>
DN PREV200400257602
TI ***VMP*** -like sequences of pathogenic ***Borrelia*** .
AU ***Norris, Steven J.*** [Inventor, Reprint Author]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]
CS Delmar, NY, USA
ASSIGNEE: Board of Regents, The University of Texas System

PI US 6719983 20040413
SO Official Gazette of the United States Patent and Trademark Office Patents, (Apr 13 2004) Vol. 1281, No. 2.
http://www.uspto.gov/web/menu/patdata.html. e-file.
ISSN: 0098-1133 (ISSN print).
DT Patent
LA English
ED Entered STN: 12 May 2004
Last Updated on STN: 12 May 2004
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
TI ***VMP*** -like sequences of pathogenic ***Borrelia*** .
AU ***Norris, Steven J.*** [Inventor, Reprint Author]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor];. . .
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
IT Major Concepts
Medical Genetics (Allied Medical Sciences); Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
Borrelia ***VMP*** -like DNA sequences

L2 ANSWER 9 OF 21 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:565053 CAPLUS <<LOGINID::20090609>>
DN 141:118336
TI Polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease
IN ***Norris, Steven J.***
PA Board of Regents, University of Texas System, USA
SO PCT Int. Appl., 182 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004058181	A2	20040715	WO 2003-US41182	20031222
WO 2004058181	A3	20050421		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ,

BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PI AU 2003299872 A1 20040722 AU 2003-299872 20031222
EP 1572714 A2 20050914 EP 2003-800145 20031222
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
US 20060240035 A1 20061026 US 2005-539956 20050617
PRAI US 2002-435077P P 20021220
WO 2003-US41182 W 20031222

AB The invention claims DNA sequences encoding variable major protein (***VMP***)-like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the prodn. of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. The invention also claims use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments, and antibodies. Examples of the invention show reactivity of human Lyme disease serum with recombinant ***Borrelia*** afzelii ***Vls*** (variable major protein-like sequence) protein ***VLS*** -BA13 and with recombinant B. garinii ***Vls*** protein ***VLS*** -BG10. Mouse anti- ***Borrelia*** burgdorferi serum also reacted in an enzyme immunoassay with the recombinant proteins ***VLS*** -BA13 and ***VLS*** -BG10. The examples also show gene organization of ***vls*** silent cassette loci from B. afzelii strain ACAI and B. garinii strain Ip90, expression of gene vlsE, and cDNA sequences of vlsE variants cloned from strains that were passaged through mice.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease

IN ***Norris, Steven J.***

AB The invention claims DNA sequences encoding variable major protein (***VMP***)-like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . . the described polypeptides, DNA segments, and antibodies. Examples of the invention show reactivity of human Lyme disease serum with recombinant ***Borrelia*** afzelii ***Vls*** (variable major protein-like sequence) protein ***VLS*** -BA13 and with recombinant B. garinii ***Vls*** protein ***VLS*** -BG10. Mouse anti- ***Borrelia*** burgdorferi serum also reacted in an enzyme immunoassay with the recombinant proteins ***VLS*** -BA13 and ***VLS*** -BG10. The examples also show gene organization of ***vls*** silent cassette loci from B. afzelii strain ACAI and B. garinii strain Ip90, expression of gene vlsE, and cDNA sequences. . .

ST DNA sequence ***Borrelia*** gene ***vls*** antigen; ***Borrelia*** gene ***vls*** diagnosis vaccine immunotherapy Lyme disease infection

IT Infection
(bacterial; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Immunoassay
(enzyme-linked immunosorbent assay; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Recombination, genetic
(gene conversion; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)
IT Diagnosis
(immunodiagnosis; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)
IT Animals
Bos taurus
Canis familiaris
Cervidae
Equus caballus
Human
Mus
(infection; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Antibodies and Immunoglobulins
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(labeled; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Antibodies and Immunoglobulins
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(monoclonal; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Antigenic variation
Blood analysis
Borrelia afzelii
Borrelia burgdorferi
Borrelia garinii
DNA sequences
Genetic polymorphism
Immunity
Immunoassay
Immunoblotting
Immunoprecipitation
Immunotherapy
Lyme disease
Molecular cloning
Nucleic acid amplification (method)
Plasmids
Protein sequences
Radioimmunoassay

Test kits
Urine analysis
cDNA sequences
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Antigens
RL: ANT (Analyte); BPN (Biosynthetic preparation); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Nucleic acids
RNA
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Antibodies and Immunoglobulins
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Escherichia coli
(recombinant host; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

IT Fever and Hyperthermia
(relapsing; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Repetitive DNA
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***vls*** silent cassettes; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***vls*** ; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic

and therapeutic uses against infection and Lyme disease)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(vlsE; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721865-74-3 721865-75-4 721865-91-4 721865-92-5
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** afzelii strain ACAI gene vls13 primer; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721865-72-1
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** burgdorferi B31 vlsE and ***vls*** silent cassette flanking direct repeat; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721865-93-6 721865-94-7 721865-95-8 721865-96-9
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** garinii strain Ip90 gene vls10 primer; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-14-5
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4470; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-15-6
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4471; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-03-2
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4540; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-11-2
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4545; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-10-1
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4548; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-12-3
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4587; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-13-4
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4588; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721862-92-6P 721862-95-9P 721863-00-9P 721863-01-0P 721863-02-1P
721863-07-6P 721863-08-7P 721863-09-8P 721863-19-0P 721863-20-3P
721863-33-8P 721863-34-9P 721863-35-0P 721863-36-1P 721863-37-2P
721863-38-3P 721863-39-4P 721863-40-7P 721863-41-8P 721863-42-9P
721863-43-0P 721863-45-2P 721863-48-5P 721863-62-3P 721863-63-4P
721863-64-5P 721863-65-6P 721863-66-7P 721863-67-8P 721863-68-9P
721863-70-3P 721863-73-6P 721863-74-7P 721865-61-8P, Antigen (plasmid pBG-10-1 gene vls10) 721865-63-0P 721865-64-1P 721865-65-2P
721865-66-3P 721865-67-4P 721865-68-5P 721865-71-0P, Antigen (plasmid pBA-13-1 gene vls13)
RL: ANT (Analyte); BPN (Biosynthetic preparation); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 511612-64-9 511612-65-0 511612-66-1 511612-67-2 511612-68-3
511612-69-4 511612-70-7 511612-71-8 511612-72-9 511612-73-0
511612-74-1 511612-75-2 511612-76-3 511612-77-4 511612-78-5
511612-79-6, Antigen (***Borrelia*** afzelii strain ACAI clone 2622 gene vlsE C-terminal fragment) 511612-80-9, Antigen (***Borrelia*** afzelii strain ACAI clone 2624a gene vlsE C-terminal fragment)
511612-81-0, Antigen (***Borrelia*** afzelii strain ACAI clone 2624b gene vlsE C-terminal fragment) 511612-82-1, Antigen (***Borrelia***

afzelii strain ACAI clone 2625 gene vlsE fragment) 511612-83-2
511612-84-3 511612-85-4 511612-86-5 511612-87-6 511612-88-7
511612-89-8 511612-90-1 511612-91-2 511612-92-3 511612-93-4
511612-94-5 511612-95-6 511612-96-7, Antigen (***Borrelia***
garinii strain Ip90 clone 17 gene vlsE fragment) 511612-97-8, Antigen (
Borrelia garinii strain Ip90 clone 20 gene vlsE fragment)
511612-98-9, Antigen (***Borrelia*** garinii strain Ip90 clone 21 gene
vlsE fragment) 511612-99-0, Antigen (***Borrelia*** garinii strain
Ip90 clone 23 gene vlsE fragment)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(amino acid sequence; polynucleotide and polypeptide sequences for
vls genes of pathogenic ***Borrelia*** and their
diagnostic
and therapeutic uses against infection and Lyme disease)
IT 721862-91-5 721862-96-0 721862-97-1 721862-98-2 721862-99-3
721863-04-3 721863-05-4 721863-06-5 721863-16-7 721863-21-4
721863-22-5 721863-23-6 721863-24-7 721863-25-8 721863-26-9
721863-27-0 721863-28-1 721863-29-2 721863-30-5 721863-31-6
721863-32-7 721863-44-1 721863-46-3 721863-47-4 721863-49-6
721863-50-9 721863-51-0 721863-52-1 721863-53-2 721863-54-3
721863-55-4 721863-56-5 721863-57-6 721863-58-7 721863-59-8
721863-60-1 721863-61-2 721863-69-0 721863-71-4 721863-72-5
721865-60-7, DNA (plasmid pBG-10-1 gene vls10) 721865-62-9, DNA (plasmid
pBA-13-1 gene vls13) 721865-69-6 721865-70-9
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic
use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
USES (Uses)
(nucleotide sequence; polynucleotide and polypeptide sequences for
vls genes of pathogenic ***Borrelia*** and their
diagnostic
and therapeutic uses against infection and Lyme disease)
IT 503713-49-3 503713-50-6 503713-51-7 503713-52-8 503713-53-9
503713-54-0 503713-55-1 503713-56-2 503713-57-3 503713-58-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(nucleotide sequence; polynucleotide and polypeptide sequences for
vls genes of pathogenic ***Borrelia*** and their
diagnostic
and therapeutic uses against infection and Lyme disease)
IT 58-85-5D, Biotin, conjugates
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN
(Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES
(Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of
pathogenic ***Borrelia*** and their diagnostic and therapeutic uses
against infection and Lyme disease)
IT 145856-09-3, GenBank L04788 391840-97-4, GenBank U76405
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(polynucleotide and polypeptide sequences for ***vls*** genes of
pathogenic ***Borrelia*** and their diagnostic and therapeutic uses
against infection and Lyme disease)
IT 721865-73-2
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological
study); USES (Uses)
(restriction endonuclease EcoRI-site linker; polynucleotide and

polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721869-20-1 721869-22-3 721869-24-5
RL: PRP (Properties)
(unclaimed nucleotide sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721869-21-2 721869-23-4
RL: PRP (Properties)
(unclaimed protein sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 116934-33-9
RL: PRP (Properties)
(unclaimed sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

L2 ANSWER 10 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 4

AN 2005:50985 BIOSIS <<LOGINID::20090609>>

DN PREV200500047406

TI Effects of vlsE complementation on the infectivity of ***Borrelia*** burgdorferi lacking the linear plasmid lp28-1.

AU Lawrenz, Matthew B.; Wooten, R. Mark; ***Norris, Steven J.*** [Reprint Author]

CS Sch MedDept Pathol and Lab Med, Univ Texas, POB 20708, Houston, TX, 77225, USA
steven.j.norris@uth.tmc.edu

SO Infection and Immunity, (November 2004) Vol. 72, No. 11, pp. 6577-6585. print.
ISSN: 0019-9567 (ISSN print).

DT Article

LA English

ED Entered STN: 26 Jan 2005
Last Updated on STN: 26 Jan 2005

AB The loss of linear plasmid lp28-1, which contains the ***vls*** antigenic variation locus, is associated with reduced infectivity of ***Borrelia*** burgdorfieri in immunocompetent mice. The recombinant shuttle vector pBBE22, which includes the virulence determinant BBE22 from lp25 and restores infectivity to readily transformable B. burgdorferi lacking lp25 and lp56, was used to determine the effect of trans expression of vlsE on virulence. Spirochetes lacking lp28-1 were complemented with the plasmid pBBE22:vlsE, containing both BBE22 and vlsE. VlsE protein produced by this construct was expressed and surface accessible in in vitro-cultured B. burgdorferi, as determined by surface proteolysis and immunoblot analysis. Clones lacking lp25 but containing lp28-1 and either pBBE22 or pBBE22:vlsE were reisolated consistently from immunocompetent mice 8 weeks after infection. In contrast, a clone lacking both lp25 and lp28-1 and complemented with pBBE22:vlsE was isolated from only a single tissue of one of six C3H/HeN mice 8 weeks postinfection. These results indicate that either an intact v/s antigenic variation locus or another determinant on lp28-1 is required to restore complete infectivity. In addition, an isogenic clone that retained lp28-1

was complemented with the v/sE shuttle plasmid and was examined for vlsE sequence variation and infectivity. Sequence variation was not observed for the shuttle plasmid, indicating that the cis arrangement of v/sE and the ***vls*** silent cassettes in lp28-1 facilitate vlsE gene conversion. Lack of vlsE sequence variation on the shuttle plasmid thus did not result in clearance of the trans-complemented strain in immunocompetent mice under the conditions tested.

TI Effects of vlsE complementation on the infectivity of ***Borrelia*** burgdorferi lacking the linear plasmid lp28-1.

AU Lawrenz, Matthew B.; Wooten, R. Mark; ***Norris, Steven J.*** [Reprint Author]

AB The loss of linear plasmid lp28-1, which contains the ***vls*** antigenic variation locus, is associated with reduced infectivity of ***Borrelia*** burgdorferi in immunocompetent mice. The recombinant shuttle vector pBBE22, which includes the virulence determinant BBE22 from lp25 and restores infectivity. . . and infectivity. Sequence variation was not observed for the shuttle plasmid, indicating that the cis arrangement of v/sE and the ***vls*** silent cassettes in lp28-1 facilitate vlsE gene conversion. Lack of vlsE sequence variation on the shuttle plasmid thus did not. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi (species): pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 11 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 5

AN 2003:153698 BIOSIS <<LOGINID::20090609>>

DN PREV200300153698

TI Characterization of the ***vls*** antigenic variation loci of the Lyme disease spirochaetes ***Borrelia*** garinii Ip90 and ***Borrelia*** afzelii ACAI.

AU Wang, Dachun; Botkin, Douglas J.; ***Norris, Steven J.*** [Reprint Author]

CS Department of Pathology and Laboratory Medicine, Medical School at Houston, University of Texas, PO Box 20708, Houston, TX, 77225-0708, USA Steven.J.Norris@uth.tmc.edu

SO Molecular Microbiology, (March 2003) Vol. 47, No. 5, pp. 1407-1417. print. ISSN: 0950-382X (ISSN print).

DT Article

LA English

ED Entered STN: 26 Mar 2003
Last Updated on STN: 26 Mar 2003

AB The ***vls*** locus of ***Borrelia*** burgdorferi B31 consists of 15 silent cassettes and one expression site (vlsE), and the presence of the encoding plasmid lp28-1 correlates with high infectivity. Recombination between the expression cassette and silent cassettes occurs in vivo, and this process may enable B. burgdorferi to evade the immune response. To determine the characteristics of the ***vls*** loci in other ***Borrelia*** strains, we have cloned and characterized the ***vls*** silent cassette loci of ***Borrelia*** garinii Ip90 and

Borrelia afzelii ACAI, consisting of 11 ***vls*** silent cassettes and 14 ***vls*** silent cassettes respectively. The silent cassettes share 90-97% nucleotide sequence identity with one another within the Ip90 ***vls*** locus and 84-91% within the ACAI ***vls*** locus. In both organisms, the silent cassettes resemble the B31 ***Vls*** sequences in overall amino acid similarity (50-65%) and in the presence of six variable regions interspersed between six relatively invariant regions. The vise expression sites of these two strains have not been isolated, but transcripts of vise were detected by reverse transcriptase-polymerase chain reaction for both Ip90 and ACAI. In addition, the occurrence of sequence variation within the vlsE cassette region of these transcripts was verified. This study indicates that the ***vls*** loci present in B. garinii Ip90 and B. afzelii ACAI have characteristics similar to those found in B. burgdorferi B31.

TI Characterization of the ***vls*** antigenic variation loci of the Lyme disease spirochaetes ***Borrelia*** garinii Ip90 and ***Borrelia*** afzelii ACAI.

AU Wang, Dachun; Botkin, Douglas J.; ***Norris, Steven J.*** [Reprint Author]

AB The ***vls*** locus of ***Borrelia*** burgdorferi B31 consists of 15 silent cassettes and one expression site (vlsE), and the presence of the encoding plasmid Ip28-1. . . in vivo, and this process may enable B. burgdorferi to evade the immune response. To determine the characteristics of the ***vls*** loci in other ***Borrelia*** strains, we have cloned and characterized the ***vls*** silent cassette loci of ***Borrelia*** garinii Ip90 and ***Borrelia*** afzelii ACAI, consisting of 11 ***vls*** silent cassettes and 14 ***vls*** silent cassettes respectively. The silent cassettes share 90-97% nucleotide sequence identity with one another within the Ip90 ***vls*** locus and 84-91% within the ACAI ***vls*** locus. In both organisms, the silent cassettes resemble the B31 ***Vls*** sequences in overall amino acid similarity (50-65%) and in the presence of six variable regions interspersed between six relatively invariant. . . the occurrence of sequence variation within the vlsE cassette region of these transcripts was verified. This study indicates that the ***vls*** loci present in B. garinii Ip90 and B. afzelii ACAI have characteristics similar to those found in B. burgdorferi B31.

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia afzelii (species): parasite, strain-ACAI
Borrelia burgdorferi (species): parasite, B31
Borrelia garinii (species): parasite, strain-Ip90
Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***vls*** gene: antigenic variation loci

L2 ANSWER 12 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2002:523404 BIOSIS <<LOGINID::20090609>>

DN PREV200200523404

TI ***VMP*** -like sequences of pathogenic ***borrelia*** .

AU ***Norris, Steven J.*** [Inventor, Reprint author]; Zhang, Jing-Ren

[Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]
CS Houston, TX, USA
ASSIGNEE: Board of Regents, The University of Texas System
PI US 6437116 20020820
SO Official Gazette of the United States Patent and Trademark Office Patents, (Aug. 20, 2002) Vol. 1261, No. 3.
http://www.uspto.gov/web/menu/patdata.html. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.
DT Patent
LA English
ED Entered STN: 9 Oct 2002
Last Updated on STN: 9 Oct 2002
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the deletion of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
TI ***VMP*** -like sequences of pathogenic ***borrelia*** .
AU ***Norris, Steven J.*** [Inventor, Reprint author]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor];. . .
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
IT Major Concepts
Infection; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
DNA sequences; ***Vmp*** -like polypeptides
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia : pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 13 OF 21 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:791027 CAPLUS <<LOGINID::20090609>>
DN 136:304895
TI Analysis of ***Borrelia*** burgdorferi vlsE gene expression and recombination in the tick vector
AU Indest, Karl J.; Howell, Jerrilyn K.; Jacobs, Mary B.; Scholl-Meeker, Dorothy; ***Norris, Steven J.*** ; Philipp, Mario T.
CS Department of Parasitology, Tulane Regional Primate Research Center, Tulane University Health Sciences Center, Covington, LA, 70433, USA
SO Infection and Immunity (2001), 69(11), 7083-7090
CODEN: INFIBR; ISSN: 0019-9567
PB American Society for Microbiology
DT Journal

LA English

AB Expression and recombination of the antigenic variation vlsE gene of the Lyme disease spirochete ***Borrelia*** burgdorferi were analyzed in the tick vector. To assess vlsE expression, Ixodes scapularis nymphs infected with the B. burgdorferi strain B31 were fed on mice for 48 or 96 h or to repletion, and then crushed and acetone fixed either immediately thereafter (ticks collected at the two earlier time points) or 4 days after repletion. Unfed nymphs also were examd. At all of the time points investigated, spirochetes were able to bind a rabbit antibody raised against the conserved invariable region 6 of VlsE, as assessed by indirect immunofluorescence, but not pre-immune serum from the same rabbit. This same antibody also bound to B31 spirochetes cultivated in vitro. Intensity of fluorescence appeared highest in cultured spirochetes, followed by spirochetes present in unfed ticks. Only a dim fluorescent signal was obsd. on spirochetes at the 48 and 96 h time points and at day 4 post-repletion. Expression of vlsE in vitro was affected by a rise in pH from 7.0 to 8.0 at 34.degree.C. Hence, vlsE expression appears to be sensitive to environmental cues of the type found in the B. burgdorferi natural history. To assess vlsE recombination, nymphs were capillary fed the B. burgdorferi B31 clonal isolate 5A3. Ticks thus infected were either left to rest for 4 wk (Group I) or fed to repletion on a mouse (Group II). The contents of each tick from both groups were cultured and 10 B. burgdorferi clones from the spirochetal isolate of each tick were obtained. The vlsE cassettes from several of these clones were amplified by PCR and sequenced. Regardless of whether the isolate was derived from Group I or Group II ticks, no changes were obsd. in the vlsE sequence. In contrast, vlsE cassettes amplified from B. burgdorferi clones derived from a mouse that was infected with B31-5A3 capillary-fed nymphs showed considerable recombination. It follows that vlsE recombination does not occur in the tick vector.

RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Analysis of ***Borrelia*** burgdorferi vlsE gene expression and recombination in the tick vector

AU Indest, Karl J.; Howell, Jerrilyn K.; Jacobs, Mary B.; Scholl-Meeker, Dorothy; ***Norris, Steven J.*** ; Philipp, Mario T.

AB Expression and recombination of the antigenic variation vlsE gene of the Lyme disease spirochete ***Borrelia*** burgdorferi were analyzed in the tick vector. To assess vlsE expression, Ixodes scapularis nymphs infected with the B. burgdorferi strain. . .

ST DNA sequence ***Borrelia*** gene vlsE mouse infection tick; ***Borrelia*** gene vlsE lipoprotein tick expression; protein sequence gene vlsE lipoprotein ***Borrelia*** ; genetic recombination ***Borrelia*** gene vlsE mouse infection tick

IT Ixodes scapularis
(anal. of ***Borrelia*** burgdorferi vlsE gene expression and recombination in tick vector)

IT Lipoproteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene vlsE, for ***Vmp*** -like sequence; partial sequence and expression in tick of ***Borrelia*** burgdorferi gene vlsE lipoprotein)

IT Development, nonmammalian postembryonic
(nymph; anal. of ***Borrelia*** burgdorferi vlsE gene expression and recombination in tick vector)

IT ***Borrelia*** burgdorferi

DNA sequences
Protein sequences
(partial sequence of ***Borrelia*** burgdorferi gene vlsE lipoprotein isolated from mouse infected by infestation with Ixodes scapularis nymphal ticks)
IT Lyme disease
Mus
Recombination, genetic
(vlsE cassettes amplified from ***Borrelia*** burgdorferi clones derived from mouse infected with B31-5A3 capillary-fed nymphs showed considerable recombination)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(vlsE; partial DNA sequence, expression and recombination in tick vector of ***Borrelia*** burgdorferi gene vlsE)
IT 411243-31-7 411243-32-8 411243-33-9 411243-34-0
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; partial sequence of ***Borrelia*** burgdorferi gene vlsE lipoprotein isolated from mouse infected by infestation with Ixodes scapularis nymphal ticks)
IT 359572-33-1, GenBank AY043397 359572-34-2, GenBank AY043398
359572-35-3, GenBank AY043399 359572-36-4, GenBank AY043400
382261-30-5, GenBank AY043401
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; partial DNA sequence, expression and recombination in tick vector of ***Borrelia*** burgdorferi gene vlsE)

L2 ANSWER 14 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 6
AN 2001:63090 BIOSIS <<LOGINID::20090609>>
DN PREV200100063090
TI Correlation between plasmid content and infectivity in ***Borrelia*** burgdorferi.
AU Purser, Joye E.; ***Norris, Steven J.*** [Reprint author]
CS Department of Pathology and Laboratory Medicine, Medical School, and Graduate School of Biomedical, University of Texas-Houston Health Science Center, Houston, TX, 77225, USA
Steven.J.Norris@uth.tmc.edu
SO Proceedings of the National Academy of Sciences of the United States of America, (December 5, 2000) Vol. 97, No. 25, pp. 13865-13870. print.
CODEN: PNASA6. ISSN: 0027-8424.
DT Article
LA English
ED Entered STN: 31 Jan 2001
Last Updated on STN: 12 Feb 2002
AB Infectivity-associated plasmids were identified in ***Borrelia*** burgdorferi B31 by using PCR to detect each of the plasmids in a panel of 19 clonal isolates. The clones exhibited high-, low-, and intermediate-infectivity phenotypes based on their frequency of isolation from needle-inoculated C3H/HeN mice. Presence or absence of 21 of the 22 plasmids was determined in each of the clones by using PCR primers specific for regions unique to each plasmid, as identified in the recently available genome sequence. Southern blot hybridization results were used

to confirm the PCR results in some cases. Plasmid lp25 exhibited a direct correlation with infectivity in that it was consistently present in all clones of high or intermediate infectivity and was absent in all low-infectivity clones. lp28-1, containing the ***vmp*** -like sequence locus, also correlated with infectivity; all clones that lacked lp28-1 but contained lp25 had an intermediate infectivity phenotype, in which infection was primarily restricted to the joints. Plasmids cp9, cp32-3, lp21, lp28-2, lp28-4, and lp56 apparently are not required for infection in this model, because clones lacking these plasmids exhibited a high-infectivity phenotype. Plasmids cp26, cp32-1, cp32-2 and/or cp32-7, cp32-4, cp32-6, cp32-8, cp32-9, lp17, lp28-3, lp36, lp38, and lp54 were consistently present in all clones examined. On the basis of these results, lp25 and lp28-1 appear to encode virulence factors important in the pathogenesis of B. burgdorferi B31.

TI Correlation between plasmid content and infectivity in ***Borrelia*** burgdorferi.

AU Purser, Joye E.; ***Norris, Steven J.*** [Reprint author]

AB Infectivity-associated plasmids were identified in ***Borrelia*** burgdorferi B31 by using PCR to detect each of the plasmids in a panel of 19 clonal isolates. The clones. . . consistently present in all clones of high or intermediate infectivity and was absent in all low-infectivity clones. lp28-1, containing the ***vmp*** -like sequence locus, also correlated with infectivity; all clones that lacked lp28-1 but contained lp25 had an intermediate infectivity phenotype, in. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi: pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 15 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 7

AN 2000:169153 BIOSIS <<LOGINID::20090609>>

DN PREV200000169153

TI Conservation and heterogeneity of vlsE among human and tick isolates of ***Borrelia*** burgdorferi.

AU Iyer, Radha; Hardham, John M.; Wormser, Gary P.; Schwartz, Ira; ***Norris, Steven J.*** [Reprint author]

CS Department of Pathology and Laboratory Medicine, University of Texas Medical School at Houston, Houston, TX, 77225, USA

SO Infection and Immunity, (March, 2000) Vol. 68, No. 3, pp. 1714-1718. print.
CODEN: INFIBR. ISSN: 0019-9567.

DT Article

LA English

ED Entered STN: 3 May 2000
Last Updated on STN: 4 Jan 2002

AB The ***vls*** (variable major protein (***VMP***)-like sequence) locus of ***Borrelia*** burgdorferi encodes an antigenic variation system that closely resembles the ***VMP*** system of relapsing fever ***borreliae*** . To determine whether ***vls*** sequences are present consistently in low-passage, infectious isolates of B.

burgdorferi, 22 blood and erythema migrans biopsy isolates from Lyme disease patients in Westchester County, New York, were examined by Southern blot and PCR analysis. Each of the strains contained a single plasmid varying in size from 21 to 38 kb that hybridized strongly with a vlsE probe based on the B. burgdorferi B31 sequence. In contrast, PCR products were obtained with only 10 of the 22 strains when primers corresponding to the 5' and 3' regions of the B31 vlsE sequence outside the variable cassette region were used. Only 2 of 16 B. burgdorferi-infected tick specimens yielded detectable PCR product. Eight of 10 strains that yielded a PCR product under these conditions were type 1 (a genotype with a high rate of dissemination), according to PCR-restriction fragment length polymorphism analysis of intergenic rDNA sequences, whereas the isolates that did not yield vlsE PCR products were either type 2 or type 3. Comparison of the sequences of cloned PCR products from the patient isolates indicated a high degree of identity to the B31 sequence, with most of the differences restricted to the hypervariable regions known to undergo sequence variation. Taken together, these results both reinforce previous evidence that ***vls*** sequences are present consistently in low-passage Lyme disease spirochetes and indicate that both highly conserved and heterogeneous subgroups exist with regard to vlsE sequences.

TI Conservation and heterogeneity of vlsE among human and tick isolates of ***Borrelia*** burgdorferi.

AU Iyer, Radha; Hardham, John M.; Wormser, Gary P.; Schwartz, Ira; ***Norris, Steven J.*** [Reprint author]

AB The ***vls*** (variable major protein (***VMP***)-like sequence) locus of ***Borrelia*** burgdorferi encodes an antigenic variation system that closely resembles the ***VMP*** system of relapsing fever ***borreliae*** . To determine whether ***vls*** sequences are present consistently in low-passage, infectious isolates of B. burgdorferi, 22 blood and erythema migrans biopsy isolates from Lyme. . . differences restricted to the hypervariable regions known to undergo sequence variation. Taken together, these results both reinforce previous evidence that ***vls*** sequences are present consistently in low-passage Lyme disease spirochetes and indicate that both highly conserved and heterogeneous subgroups exist with. . .

IT Major Concepts
Infection

IT Diseases
Lyme disease: bacterial disease
Lyme Disease (MeSH)

IT Chemicals & Biochemicals
Borrelia burgdorferi ***vls*** gene; ***Borrelia*** burgdorferi vlsE gene

ORGN . . .

Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi: pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 16 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on

STN DUPLICATE 8
AN 1998:393355 BIOSIS <<LOGINID::20090609>>
DN PREV199800393355
TI Genetic variation of the ***Borrelia*** burgdorferi gene vlsE involves cassette-specific, segmental gene conversion.
AU Zhang, Jing-Ren; ***Norris, Steven J.*** [Reprint author]
CS Dep. Pathol. Lab. Med., Univ. Tex. Med. Sch., 6431 Fannin, Houston, TX 77030, USA
SO Infection and Immunity, (Aug., 1998) Vol. 66, No. 8, pp. 3698-3704. print. CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 10 Sep 1998
Last Updated on STN: 10 Sep 1998
AB The Lyme disease spirochete ***Borrelia*** burgdorferi possesses 15 silent ***vls*** cassettes and a ***vls*** expression site (vlsE) encoding a surface-exposed lipoprotein. Segments of the silent ***vls*** cassettes have been shown to recombine with the vlsE cassette region in the mammalian host, resulting in combinatorial antigenic variation. Despite promiscuous recombination within the vlsE cassette region, the 5' and 3' coding sequences of vlsE that flank the cassette region are not subject to sequence variation during these recombination events. The segments of the silent ***vls*** cassettes recombine in the vlsE cassette region through a unidirectional process such that the sequence and organization of the silent ***vls*** loci are not affected. As a result of recombination, the previously expressed segments are replaced by incoming segments and apparently degraded. These results provide evidence for a gene conversion mechanism in VlsE antigenic variation.
TI Genetic variation of the ***Borrelia*** burgdorferi gene vlsE involves cassette-specific, segmental gene conversion.
AU Zhang, Jing-Ren; ***Norris, Steven J.*** [Reprint author]
AB The Lyme disease spirochete ***Borrelia*** burgdorferi possesses 15 silent ***vls*** cassettes and a ***vls*** expression site (vlsE) encoding a surface-exposed lipoprotein. Segments of the silent ***vls*** cassettes have been shown to recombine with the vlsE cassette region in the mammalian host, resulting in combinatorial antigenic variation.. . . that flank the cassette region are not subject to sequence variation during these recombination events. The segments of the silent ***vls*** cassettes recombine in the vlsE cassette region through a unidirectional process such that the sequence and organization of the silent ***vls*** loci are not affected. As a result of recombination, the previously expressed segments are replaced by incoming segments and apparently. . .
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia -burgdorferi
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 17 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 9
AN 1998:393354 BIOSIS <<LOGINID::20090609>>
DN PREV199800393354

TI Kinetics and in vivo induction of genetic variation of vlsE in ***Borrelia*** burgdorferi.
AU Zhang, Jing-Ren; ***Norris, Steven J.*** [Reprint author]
CS Dep. Pathol. Lab. Med., Univ. Tex. Med. Sch., 6431 Fannin, Houston, TX 77030, USA
SO Infection and Immunity, (Aug., 1998) Vol. 66, No. 8, pp. 3689-3697. print. CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 10 Sep 1998
Last Updated on STN: 10 Sep 1998
AB The Lyme disease agent, ***Borrelia*** burgdorferi, is able to persistently infect humans and animals for months or years in the presence of an active immune response. It is not known how the organisms survive immune attack in the mammalian host. vlsE, a gene localized near one end of linear plasmid lp28-1 and encoding a surface-exposed lipoprotein in B. burgdorferi B31, was shown recently to undergo extensive genetic and antigenic variation within 28 days of initial infection in C3H/HeN mice. In this study, we examined the kinetics of vlsE sequence variation in C3H/HeN mice at 4, 7, 14, 21, and 28 days and at 7 and 12 months postinfection. Sequence changes were detected by PCR amplification and sequence analysis as early as 4 days postinfection and accumulated progressively in both C3H/HeN and CB-17 severe combined immunodeficient (SCID) mice throughout the course of infection. The sequence changes were consistent with sequential recombination of segments from multiple silent ***vls*** cassette sites into the vlsE expression site. No vlsE sequence changes were detected in organisms cultured in vitro for up to 84 days. These results indicate that vlsE recombination is induced by a factor(s) present in the mammalian host, independent of adaptive immune responses. The possible inducing conditions appear to be present in various tissue sites because isolates from multiple tissues showed similar degrees of sequence variation. The rate of accumulation of predicted amino acid changes was higher in the immunologically intact C3H/HeN mice than in SCID mice, a finding consistent with immune selection of VlsE variants.
TI Kinetics and in vivo induction of genetic variation of vlsE in ***Borrelia*** burgdorferi.
AU Zhang, Jing-Ren; ***Norris, Steven J.*** [Reprint author]
AB The Lyme disease agent, ***Borrelia*** burgdorferi, is able to persistently infect humans and animals for months or years in the presence of an active immune. . . . (SCID) mice throughout the course of infection. The sequence changes were consistent with sequential recombination of segments from multiple silent ***vls*** cassette sites into the vlsE expression site. No vlsE sequence changes were detected in organisms cultured in vitro for up. . .
ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia -burgdorferi
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 18 OF 21 CAPLUS COPYRIGHT 2009 ACS on STN

AN 1997:579836 CAPLUS <<LOGINID::20090609>>
DN 127:189742
OREF 127:36809a,36812a
TI ***Vmp*** -like sequences of pathogenic ***Borrelia***
IN ***Norris, Steven J.*** ; Zhang, Jing-ren; Hardham, John M.; Howell, Jerrilyn K.; Barbour, Alan G.; Weinstock, George M.
PA Board of Regents, the University of Texas System, USA; Norris, Steven J.; Zhang, Jing-Ren; Hardham, John M.; Howell, Jerrilyn K.; Barbour, Alan G.; Weinstock, George M.
SO PCT Int. Appl., 130 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9731123	A1	19970828	WO 1997-US2952	19970220
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9721915	A	19970910	AU 1997-21915	19970220
	EP 894143	A1	19990203	EP 1997-914794	19970220
	EP 894143	B1	20050810		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	AT 301716	T	20050815	AT 1997-914794	19970220
	EP 1589109	A2	20051026	EP 2005-10338	19970220
	EP 1589109	A3	20051116		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	US 6437116	B1	20020820	US 1999-125619	19990127
	US 20030092903	A1	20030515	US 2002-143024	20020731
	US 6740744	B2	20040525		
	US 20030060618	A1	20030327	US 2002-222162	20020816
	US 6878816	B2	20050412		
	US 20040044192	A1	20040304	US 2002-222566	20020816
	US 6719983	B2	20040413		
	US 20040214225	A1	20041028	US 2004-852555	20040524
	US 7135176	B2	20061114		
	US 20070117970	A1	20070524	US 2006-501166	20060807
PRAI	US 1996-12028P	P	19960221		
	EP 1997-914794	A3	19970220		
	WO 1997-US2952	W	19970220		
	US 1999-125619	A3	19990127		
	US 2002-143024	A3	20020731		
	US 2002-222162	A3	20020816		
	US 2004-852555	A3	20040524		

AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the prodn. of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the

nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.

RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI ***Vmp*** -like sequences of pathogenic ***Borrelia***

IN ***Norris, Steven J.*** ; Zhang, Jing-ren; Hardham, John M.; Howell, Jerrilyn K.; Barbour, Alan G.; Weinstock, George M.

AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .

ST variable major protein gene ***Borrelia***

IT ***Borrelia*** burgdorferi
(***Vmp*** -like sequences of pathogenic ***Borrelia***)

IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(gene vlsE; ***Vmp*** -like sequences of pathogenic ***Borrelia***)

IT 189614-97-9, DNA (***Borrelia*** burgdorferi strain B31 clone 5A3 gene vlsE plus flanks)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(***Vmp*** -like sequences of pathogenic ***Borrelia***)

IT 189833-73-6, Protein (***Borrelia*** burgdorferi strain B31 clone 5A3 gene vlsE)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(***Vmp*** -like sequences of pathogenic ***Borrelia***)

L2 ANSWER 19 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 10

AN 1997:225972 BIOSIS <<LOGINID::20090609>>

DN PREV199799517688

TI Antigenic variation in Lyme disease ***Borreliae*** by promiscuous recombination of ***VMP*** -like sequence cassettes.

AU Zhang, Jing-Ren [Reprint author]; Hardham, John M.; Barbour, Alan G.; ***Norris, Steven J.***

CS Dep. Pathol., Univ. Texas Med. Sch. Houston, Houston, TX 77030, USA

SO Cell, (1997) Vol. 89, No. 2, pp. 275-285.
CODEN: CELLB5. ISSN: 0092-8674.

DT Article

LA English

ED Entered STN: 22 May 1997
Last Updated on STN: 22 May 1997

AB We have identified and characterized an elaborate genetic system in the Lyme disease spirochete ***Borrelia*** burgdorferi that promotes extensive antigenic variation of a surface-exposed lipoprotein, VlsE. A 28 kb linear plasmid of B. burgdorferi B31 (lp28-1) was found to contain a ***vmp*** -like sequence (***vls***) locus that closely resembles the variable major protein (***vmp***) system for antigenic variation of relapsing fever organisms. Portions of several of the 15 nonexpressed (silent) ***vls*** cassette sequences located upstream of vlsE recombined into the central vlsE cassette region during infection of

C3H/HeN mice, resulting in antigenic variation of the expressed lipoprotein. This combinatorial variation could potentially produce millions of antigenic variants in the mammalian host.

TI Antigenic variation in Lyme disease ***Borreliae*** by promiscuous recombination of ***VMP*** -like sequence cassettes.

AU Zhang, Jing-Ren [Reprint author]; Hardham, John M.; Barbour, Alan G.; ***Norris, Steven J.***

AB We have identified and characterized an elaborate genetic system in the Lyme disease spirochete ***Borrelia*** burgdorferi that promotes extensive antigenic variation of a surface-exposed lipoprotein, VlsE. A 28 kb linear plasmid of B. burgdorferi B31 (lp28-1) was found to contain a ***vmp*** -like sequence (***vls***) locus that closely resembles the variable major protein (***vmp***) system for antigenic variation of relapsing fever organisms. Portions of several of the 15 nonexpressed (silent) ***vls*** cassette sequences located upstream of vlsE recombined into the central vlsE cassette region during infection of C3H/HeN mice, resulting in. . .

IT Miscellaneous Descriptors
ANTIGENIC VARIATION; BACTERIAL DISEASE; COMBINATORIAL VARIATION; C3H/HEN; INFECTION; LYME DISEASE; MOLECULAR GENETICS; PATHOGEN; PROMISCUOUS RECOMBINATION; SURFACE-EXPOSED LIPOPROTEIN; VLSE; ***VMP*** -LIKE SEQUENCE CASSETTES

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 20 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 1997:282165 BIOSIS <<LOGINID::20090609>>

DN PREV199799581368

TI Antigenic variation in Lyme disease spirochetes by promiscuous recombination of ***vmp*** -like sequence cassettes.

AU Zhang, Jing-Ren [Reprint author]; Hardham, John M.; Barbour, Alan G.; ***Norris, Steven J.***

CS Dep. Pathol. Lab. Med., Univ. Texas Med. Sch., Houston, TX, USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (1997) Vol. 97, No. 0, pp. 103.
Meeting Info.: 97th General Meeting of the American Society for Microbiology. Miami Beach, Florida, USA. May 4-8, 1997.
ISSN: 1060-2011.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)

LA English

ED Entered STN: 3 Jul 1997
Last Updated on STN: 3 Jul 1997

TI Antigenic variation in Lyme disease spirochetes by promiscuous recombination of ***vmp*** -like sequence cassettes.

AU Zhang, Jing-Ren [Reprint author]; Hardham, John M.; Barbour, Alan G.;

Norris, Steven J.

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L2 ANSWER 21 OF 21 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 11

AN 1994:345519 BIOSIS <<LOGINID::20090609>>

DN PREV199497358519

TI A family of surface-exposed proteins of 20 kilodaltons in the genus ***Borrelia*** .

AU Carter, Carol J.; Bergstrom, Sven; ***Norris, Steven J.*** ; Barbour, Alan G. [Reprint author]

CS Dep. Microbiol. and Med., Univ. Texas Health Sci. Cent., San Antonio, TX 78284-7758, USA

SO Infection and Immunity, (1994) Vol. 62, No. 7, pp. 2792-2799.
CODEN: INFIBR. ISSN: 0019-9567.

DT Article

LA English

OS Genbank-L24911

ED Entered STN: 8 Aug 1994
Last Updated on STN: 1 Sep 1994

AB Relapsing fever and Lyme disease spirochetes of the genus ***Borrelia*** display at their surfaces abundant lipoproteins: ***Vmp*** proteins in ***Borrelia*** hermsii and Osp proteins in ***Borrelia*** burgdorferi. ***Vmp*** and Osp proteins largely determine serotype specificity, and neutralizing antibodies of infected or immunized animals are directed at them. For the present study, we examined B. hermsii serotype 33, which is unique among strain HS1 serotypes in the low frequency of switches to other serotypes during infections and in vitro cultivation. Failing to clone the complete ***vmp33*** gene, we accomplished its further characterization by (i) determining three partial amino acid sequences, (ii) designing oligonucleotide primers based on these amino acid sequences, (iii) cloning and sequencing the central portion of ***vmp33*** , and (iv) using outwardly directed primers and the inverse PCR to clone the 5' and 3' ends of the gene and flanking regions. The transcriptional start site was identified by primer extension analysis. ***Vmp33*** was a polypeptide of 211 amino acids; the three partial amino acid sequences were identified in the open reading frame. ***Vmp33*** was found to be more similar to other 20-kDa ***Vmp*** proteins of B. hermsii and to OspC proteins of B. burgdorferi than t was to 35- to 39-kDa ***Vmp*** proteins of the same strain. Moreover, OspC proteins were more similar to ***Vmp33*** than they were to OspA, -B, or -D proteins of B. burgdorferi. These sequence similarities were consistent with Western blot (immunoblot) findings of crossreactions between ***Vmp33*** and OspC with anti- ***Vmp33*** and anti-OspC sera. The promoter for the expressed ***vmp33*** gene was found to be different from the expression site for other active ***vmp*** genes characterized to date. These results indicate that ***Vmp33*** and other small ***Vmp*** 's belong with OspC to a

genus-wide family of 20-kDa proteins and that expression of these proteins may be coordinated with expression of other ***Vmp*** and Osp proteins in ***Borrelia*** spp.

TI A family of surface-exposed proteins of 20 kilodaltons in the genus ***Borrelia*** .

AU Carter, Carol J.; Bergstrom, Sven; ***Norris, Steven J.*** ; Barbour, Alan G. [Reprint author]

AB Relapsing fever and Lyme disease spirochetes of the genus ***Borrelia*** display at their surfaces abundant lipoproteins: ***Vmp*** proteins in ***Borrelia*** hermsii and Osp proteins in ***Borrelia*** burgdorferi. ***Vmp*** and Osp proteins largely determine serotype specificity, and neutralizing antibodies of infected or immunized animals are directed at them. For. . . in the low frequency of switches to other serotypes during infections and in vitro cultivation. Failing to clone the complete ***vmp33*** gene, we accomplished its further characterization by (i) determining three partial amino acid sequences, (ii) designing oligonucleotide primers based on these amino acid sequences, (iii) cloning and sequencing the central portion of ***vmp33*** , and (iv) using outwardly directed primers and the inverse PCR to clone the 5' and 3' ends of the gene and flanking regions. The transcriptional start site was identified by primer extension analysis. ***Vmp33*** was a polypeptide of 211 amino acids; the three partial amino acid sequences were identified in the open reading frame. ***Vmp33*** was found to be more similar to other 20-kDa ***Vmp*** proteins of B. hermsii and to OspC proteins of B. burgdorferi than t was to 35- to 39-kDa ***Vmp*** proteins of the same strain. Moreover, OspC proteins were more similar to ***Vmp33*** than they were to OspA, -B, or -D proteins of B. burgdorferi. These sequence similarities were consistent with Western blot (immunoblot) findings of crossreactions between ***Vmp33*** and OspC with anti- ***Vmp33*** and anti-OspC sera. The promoter for the expressed ***vmp33*** gene was found to be different from the expression site for other active ***vmp*** genes characterized to date. These results indicate that ***Vmp33*** and other small ***Vmp*** 's belong with OspC to a genus-wide family of 20-kDa proteins and that expression of these proteins may be coordinated with expression of other ***Vmp*** and Osp proteins in ***Borrelia*** spp.

IT . . .
sequence data; nucleotide sequence; L24911: Genbank

IT Miscellaneous Descriptors
CLONING STRATEGY; HOMOLOGY; METHOD; OSPC PROTEIN; PROMOTER ANALYSIS; TRANSCRIPTION START SITE; ***VMP33*** GENE

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi
Borrelia hermsii

Taxa Notes
Bacteria, Eubacteria, Microorganisms

=> s borreli? and (VMP? or vls)
L3 337 BORRELI? AND (VMP? OR VLS)

=> dup rem l3

PROCESSING COMPLETED FOR L3
L4 87 DUP REM L3 (250 DUPLICATES REMOVED)

=> d bib ab kwic 1-
YOU HAVE REQUESTED DATA FROM 87 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 1
AN 2009:232172 BIOSIS <<LOGINID::20090609>>
DN PREV200900232172
TI Detailed Analysis of Sequence Changes Occurring during vlsE Antigenic Variation in the Mouse Model of ***Borrelia*** burgdorferi Infection.
AU Coutte, Loic [Reprint Author]; Botkin, Douglas J.; Gao, Lihui; Norris, Steven J.
CS Inst Biol Lille, Lille, France
Steven.J.Norris@uth.tmc.edu
SO PLoS Pathogens, (FEB 2009) Vol. 5, No. 2, pp. Article No.: e1000293. http://www.plospathogens.org.
ISSN: 1553-7366. E-ISSN: 1553-7374.
DT Article
LA English
ED Entered STN: 1 Apr 2009
Last Updated on STN: 1 Apr 2009
AB Lyme disease ***Borrelia*** can infect humans and animals for months to years, despite the presence of an active host immune response. The ***vls*** antigenic variation system, which expresses the surface-exposed lipoprotein VlsE, plays a major role in B. burgdorferi immune evasion. Gene conversion between ***vls*** silent cassettes and the vlsE expression site occurs at high frequency during mammalian infection, resulting in sequence variation in the VlsE product. In this study, we examined vlsE sequence variation in B. burgdorferi B31 during mouse infection by analyzing 1,399 clones isolated from bladder, heart, joint, ear, and skin tissues of mice infected for 4 to 365 days. The median number of codon changes increased progressively in C3H/HeN mice from 4 to 28 days post infection, and no clones retained the parental vlsE sequence at 28 days. In contrast, the decrease in the number of clones with the parental vlsE sequence and the increase in the number of sequence changes occurred more gradually in severe combined immunodeficiency (SCID) mice. Clones containing a stop codon were isolated, indicating that continuous expression of full-length VlsE is not required for survival in vivo; also, these clones continued to undergo vlsE recombination. Analysis of clones with apparent single recombination events indicated that recombinations into vlsE are nonselective with regard to the silent cassette utilized, as well as the length and location of the recombination event. Sequence changes as small as one base pair were common. Fifteen percent of recovered vlsE variants contained "template-independent'' sequence changes, which clustered in the variable regions of vlsE. We hypothesize that the increased frequency and complexity of vlsE sequence changes observed in clones recovered from immunocompetent mice (as compared with SCID mice) is due to rapid clearance of relatively invariant clones by variable region-specific anti-VlsE antibody responses.
TI Detailed Analysis of Sequence Changes Occurring during vlsE Antigenic Variation in the Mouse Model of ***Borrelia*** burgdorferi Infection.
AB Lyme disease ***Borrelia*** can infect humans and animals for months to years, despite the presence of an active host immune response. The ***vls*** antigenic variation system, which expresses the surface-exposed lipoprotein VlsE, plays a major role in B. burgdorferi

immune evasion. Gene conversion between ***vls*** silent cassettes and the vlsE expression site occurs at high frequency during mammalian infection, resulting in sequence variation in the. . .

IT . . .
system; bladder: excretory system; ear: sensory system; joint: skeletal system; skin tissue: integumentary system

IT Diseases
Lyme disease: bacterial disease, ***Borrelia*** burgdorferi infection

IT Chemicals & Biochemicals
antibody

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi (species): pathogen, strain-B31

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 2 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 2

AN 2008:2678 BIOSIS <<LOGINID::20090609>>

DN PREV200800010948

TI The role of VlsE antigenic variation in the Lyme disease spirochete: persistence through a mechanism that differs from other pathogens.

AU Bankhead, Troy; Chaconas, George [Reprint Author]

CS Univ Calgary, Dept Biochem and Mol Biol, Calgary, AB T2N 4N1, Canada
chaconas@ucalgary.ca

SO Molecular Microbiology, (SEP 2007) Vol. 65, No. 6, pp. 1547-1558.
CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

ED Entered STN: 12 Dec 2007
Last Updated on STN: 12 Dec 2007

AB The linear plasmid, lp28-1, is required for persistent infection by the Lyme disease spirochete, ***Borrelia*** burgdorferi. This plasmid contains the ***vls*** antigenic variation locus, which has long been thought to be important for immune evasion. However, the role of the ***vls*** locus as a virulence factor during mammalian infection has not
been clearly defined. We report the successful removal of the ***vls*** locus through telomere resolvase-mediated targeted deletion, and demonstrate the absolute requirement of this lp28-1 component for persistence in the mouse host. Moreover, successful infection of C3H/HeN mice with an lp28-1 plasmid in which the left portion was deleted excludes participation of other lp28-1 non- ***vls*** genes in spirochete virulence, persistence and the process of recombinational switching at vlsE. Data are also presented that cast doubt on an immune evasion mechanism whereby VlsE directly masks other surface antigens similar to what has been observed for several other pathogens that undergo recombinational antigenic variation.

AB The linear plasmid, lp28-1, is required for persistent infection by the Lyme disease spirochete, ***Borrelia*** burgdorferi. This plasmid contains the ***vls*** antigenic variation locus, which has long been

thought to be important for immune evasion. However, the role of the ***vls*** locus as a virulence factor during mammalian infection has not been clearly defined. We report the successful removal of the ***vls*** locus through telomere resolvase-mediated targeted deletion, and demonstrate the absolute requirement of this lp28-1 component for persistence in the mouse. . . . infection of C3H/HeN mice with an lp28-1 plasmid in which the left portion was deleted excludes participation of other lp28-1 non- ***vls*** genes in spirochete virulence, persistence and the process of recombinational switching at vlsE. Data are also presented that cast doubt. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi (species): pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Borrelia*** burgdorferi ***vls*** gene (Spirochaetaceae)

L4 ANSWER 3 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2007:587055 BIOSIS <<LOGINID::20090609>>

DN PREV200700592427

TI Gene conversion is a convergent strategy for pathogen antigenic variation.

AU Palmer, Guy H. [Reprint Author]; Brayton, Kelly A.

CS Washington State Univ, Programs Vector Borne Dis and Genom, Pullman, WA 99164 USA
gpalmer@vetmed.wsu.edu

SO Trends in Parasitology, (SEP 2007) Vol. 23, No. 9, pp. 408-413.
ISSN: 1471-4922.

DT Article
General Review; (Literature Review)

LA English

ED Entered STN: 21 Nov 2007
Last Updated on STN: 21 Nov 2007

AB Recent studies on three unrelated vector-borne pathogens, Anaplasma marginale, ***Borrelia*** hermsii and Trypanosoma brucei, illustrate the central importance of gene conversion as a mechanism for antigenic variation, which results in subsequent evasion of the immune response and persistence in the reservoir host. The combination of genome sequence data and in vivo studies tracking variant emergence not only provides insight into the genetic mechanisms for variant generation and hierarchy in variant expression but also highlights gaps in our knowledge regarding variant capacity and usage in vivo.

AB Recent studies on three unrelated vector-borne pathogens, Anaplasma marginale, ***Borrelia*** hermsii and Trypanosoma brucei, illustrate the central importance of gene conversion as a mechanism for antigenic variation, which results in. . .

IT . . .
Population Genetics (Population Studies)

IT Diseases
Anaplasma marginale infection: parasitic disease

IT Diseases
Trypanosoma brucei infection: parasitic disease

IT Diseases
Borrelia hermsii infection: parasitic disease
ORGN . . .
pathogen
Taxa Notes
Animals, Invertebrates, Microorganisms, Protozoans
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia hermsii (species): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***Borrelia*** hermsii ***vmp*** gene (Spirochaetaceae): expression; Trypanosoma brucei vsg gene (Flagellata): expression; Anaplasma marginale msp2 gene (Anaplasmataceae): expression

L4 ANSWER 4 OF 87 CABA COPYRIGHT 2009 CABI on STN DUPLICATE 3
AN 2007:261701 CABA <<LOGINID::20090609>>
DN 20073270507
TI ***Borrelia*** burgdorferi adhesins identified using in vivo phage display
AU Antonara, S.; Chafel, R. M.; LaFrance, M.; Coburn, J.
CS Graduate Program in Molecular Microbiology, Tufts University Sackler School of Graduate Biomedical Sciences, Boston, Massachusetts, USA. jcoburn@tufts-nemc.org
SO Molecular Microbiology, (2007) Vol. 66, No. 1, pp. 262-276. many ref.
Publisher: Blackwell Publishing. Oxford
ISSN: 0950-382X
URL: http://www.blackwell-synergy.com/loi/mmi
DOI: 10.1111/j.1365-2958.2007.05924.x
CY United Kingdom
DT Journal
LA English
ED Entered STN: 7 Dec 2007
Last Updated on STN: 7 Dec 2007
AB ***Borrelia*** burgdorferi, the agent of Lyme disease, disseminates from the site of deposition by Ixodes ticks to cause systemic infection. Dissemination occurs through the circulation and through tissue matrices, but the B. burgdorferi molecules that mediate interactions with the endothelium in vivo have not yet been identified. In vivo selection of filamentous phage expressing B. burgdorferi protein fragments on the phage surface identified several new candidate adhesins, and verified the activity of one adhesin that had been previously characterized in vitro. P66, a B. burgdorferi ligand for [beta]3-chain integrins, OspC, a protein that is essential for the establishment of infection in mammals, and ***Vls*** , a protein that undergoes antigenic variation in the mammal, were all selected for binding to the murine endothelium in vivo. Additional B. burgdorferi proteins for which no functions have been identified, including all four members of the OspF family and BmpD, were identified as candidate adhesins. The use of in vivo phage display is one approach to the identification of adhesins in pathogenic bacteria that are not easily grown in the laboratory, or for which genetic manipulations are not straightforward.
TI ***Borrelia*** burgdorferi adhesins identified using in vivo phage display.

AB ***Borrelia*** burgdorferi, the agent of Lyme disease, disseminates from the site of deposition by Ixodes ticks to cause systemic infection. Dissemination. . . B. burgdorferi ligand for [beta]3-chain integrins, OspC, a protein that is essential for the establishment of infection in mammals, and ***Vls*** , a protein that undergoes antigenic variation in the mammal, were all selected for binding to the murine endothelium in vivo.. . .
BT ***Borrelia*** ; Spirochaetaceae; Spirochaetales; Gracilicutes; bacteria; prokaryotes; Muridae; rodents; mammals; vertebrates; Chordata; animals; small mammals; eukaryotes
ST lyme ***borreliosis***
ORGN ***Borrelia*** burgdorferi; Murinae

L4 ANSWER 5 OF 87 MEDLINE on STN
AN 2006382551 MEDLINE <<LOGINID::20090609>>
DN PubMed ID: 16796669
TI Antigenic variation with a twist--the ***Borrelia*** story.
AU Norris Steven J
CS Department of Pathology. University of Texas Medical School at Houston, PO Box 20708, Houston, TX 77225-0708, USA.. Steven.J.Norris@uth.tmc.edu
NC R01 AI37277 (United States NIAID NIH HHS)
SO Molecular microbiology, (2006 Jun) Vol. 60, No. 6, pp. 1319-22.
Journal code: 8712028. ISSN: 0950-382X.
CY England: United Kingdom
DT Commentary
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
LA English
FS Priority Journals
EM 200608
ED Entered STN: 27 Jun 2006
Last Updated on STN: 23 Aug 2006
Entered Medline: 22 Aug 2006
AB A common mechanism of immune evasion in pathogenic bacteria and protozoa is antigenic variation, in which genetic or epigenetic changes result in rapid, sequential shifts in a surface-exposed antigen. In this issue of Molecular Microbiology, Dai et al. provide the most complete description to date of the vlp/vsp antigenic variation system of the relapsing fever spirochaete, ***Borrelia*** hermsii. This elaborate, plasmid-encoded system involves an expression site that can acquire either variable large protein (vlp) or variable small protein (vsp) surface lipoprotein genes from 59 different archival copies. The archival vlp and vsp genes are arranged in clusters on at least five different plasmids. Gene conversion occurs through recombination events at upstream homology sequences (UHS) found in each gene copy, and at downstream homology sequences (DHS) found periodically among the vlp/vsp archival genes. Previous studies have shown that antigenic variation in relapsing fever ***Borrelia*** not only permits the evasion of host antibody responses, but can also result in changes in neurotropism and other pathogenic properties. The vlsE antigenic variation locus of Lyme disease spirochaetes, although similar in sequence to the relapsing fever vlp genes, has evolved a completely different antigenic variation mechanism involving segmental recombination from a contiguous array of ***vls*** silent cassettes. These two systems thus appear to represent divergence from a common precursor followed by functional convergence to create two distinct antigenic variation processes.
TI Antigenic variation with a twist--the ***Borrelia*** story.

AB . . . et al. provide the most complete description to date of the vlp/vsp antigenic variation system of the relapsing fever spirochaete, ***Borrelia*** hermsii. This elaborate, plasmid-encoded system involves
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CT *Antigenic Variation: GE, genetics
*Antigens, Bacterial: GE, genetics
*** Borrelia: GE, genetics***
****Borrelia: IM, immunology***

L4 ANSWER 6 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:87547 BIOSIS <<LOGINID::20090609>>
DN PREV200700093298
TI ***VMP*** -like sequences of pathogenic ***Borrelia*** .
AU Anonymous; Norris, Steven J. [Inventor]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]
CS Houston, TX USA
ASSIGNEE: Board of Regents The University of Texas System
PI US 07135176 20061114
SO Official Gazette of the United States Patent and Trademark Office Patents, (NOV 14 2006)
CODEN: OGUPE7. ISSN: 0098-1133.
DT Patent
LA English
ED Entered STN: 31 Jan 2007
Last Updated on STN: 31 Jan 2007
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
TI ***VMP*** -like sequences of pathogenic ***Borrelia*** .
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
IT Major Concepts
Pharmacology; Clinical Immunology (Human Medicine, Medical Sciences); Infection
IT Chemicals & Biochemicals
Borrelia ***VMP*** -like DNA sequences: diagnostic-drug, immunostimulant-drug, immunologic-drug

L4 ANSWER 7 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 4
AN 2006:570967 BIOSIS <<LOGINID::20090609>>
DN PREV200600576492
TI Transcriptional regulation of the ***Borrelia*** burgdorferi antigenically variable VlsE surface protein.
AU Bykowski, Tomasz; Babb, Kelly; von Lackum, Kate; Riley, Sean P.; Norris, Steven J.; Stevenson, Brian [Reprint Author]
CS Univ Kentucky, Coll Med, Dept Microbiol Mol Genet and Immunol, Albert B Chandler Med Ctr, MS 415, Lexington, KY 40536 USA
brian.stevenson@uky.edu
SO Journal of Bacteriology, (JUL 2006) Vol. 188, No. 13, pp. 4879-4889.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 1 Nov 2006
Last Updated on STN: 1 Nov 2006
AB The Lyme disease agent ***Borrelia*** burgdorferi can persistently infect humans and other animals despite host active immune responses. This is facilitated, in part, by the vis locus, a complex system consisting of the vlsE expression site and an adjacent set of 11 to 15 silent ***vls*** cassettes. Segments of nonexpressed cassettes recombine with the vlsE region during infection of mammalian hosts, resulting in combinatorial antigenic variation of the VlSE outer surface protein. We now demonstrate that synthesis of VlsE is regulated during the natural mammal-tick infectious cycle, being activated in mammals but repressed during tick colonization. Examination of cultured B. burgdorferi cells indicated that the spirochete controls vlsE transcription levels in response to environmental cues. Analysis of PvlsE::gfp fusions in B. burgdorferi indicated that VlsE production is controlled at the level of transcriptional initiation, and regions of 5' DNA involved in the regulation were identified. Electrophoretic mobility shift assays detected qualitative and quantitative changes in patterns of protein-DNA complexes formed between the vlsE promoter and cytoplasmic proteins, suggesting the involvement of DNA-binding proteins in the regulation of vlsE, with at least one protein acting as a transcriptional activator.
TI Transcriptional regulation of the ***Borrelia*** burgdorferi antigenically variable VlsE surface protein.
AB The Lyme disease agent ***Borrelia*** burgdorferi can persistently infect humans and other animals despite host active immune responses. This is facilitated, in part, by the. . . vis locus, a complex system consisting of the vlsE expression site and an adjacent set of 11 to 15 silent ***vls*** cassettes. Segments of nonexpressed cassettes recombine with the vlsE region during infection of mammalian hosts, resulting in combinatorial antigenic variation. . .
ORGN . . .
Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi (species): pathogen
Taxa Notes

Bacteria, Eubacteria, Microorganisms
GEN ***Borrelia*** burgdorferi vlsE gene (Spirochaetaceae): expression

L4 ANSWER 8 OF 87 CABA COPYRIGHT 2009 CABI on STN DUPLICATE 5
AN 2006:126465 CABA <<LOGINID::20090609>>
DN 20063098478
TI Antigenic variation with a twist - the ***Borrelia*** story
AU Norris, S. J.
CS Department of Pathology & Laboratory Medicine, University of Texas Medical School at Houston, PO Box 20708, Houston, TX 77225-0708, USA. Steven.J.Norris@uth.tmc.edu
SO Molecular Microbiology, (2006) Vol. 60, No. 6, pp. 1319-1322. 20 ref.
Publisher: Blackwell Publishing. Oxford
ISSN: 0950-382X
URL: http://www.blackwell-synergy.com/servlet/useragent?func=showIssues&code=mmi
DOI: 10.1111/j.1365-2958.2006.05204.x
CY United Kingdom
DT Journal
LA English
ED Entered STN: 3 Aug 2006
Last Updated on STN: 3 Aug 2006
AB A common mechanism of immune evasion in pathogenic bacteria and protozoa is antigenic variation, in which genetic or epigenetic changes result in rapid, sequential shifts in a surface-exposed antigen. In this issue of Molecular Microbiology, Dai et al. provide the most complete description to date of the vlp/vsp antigenic variation system of the relapsing fever spirochaete, ***Borrelia*** hermsii. This elaborate, plasmid-encoded system involves an expression site that can acquire either variable large protein (vlp) or variable small protein (vsp) surface lipoprotein genes from 59 different archival copies. The archival vlp and vsp genes are arranged in clusters on at least five different plasmids. Gene conversion occurs through recombination events at upstream homology sequences (UHS) found in each gene copy, and at downstream homology sequences (DHS) found periodically among the vlp/vsp archival genes. Previous studies have shown that antigenic variation in relapsing fever ***Borrelia*** not only permits the evasion of host antibody responses, but can also result in changes in neurotropism and other pathogenic properties. The vlsE antigenic variation locus of Lyme disease spirochaetes, although similar in sequence to the relapsing fever vlp genes, has evolved a completely different antigenic variation mechanism involving segmental recombination from a contiguous array of ***vls*** silent cassettes. These two systems thus appear to represent divergence from a common precursor followed by functional convergence to create two distinct antigenic variation processes.
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AB . . . et al. provide the most complete description to date of the vlp/vsp antigenic variation system of the relapsing fever spirochaete, ***Borrelia*** hermsii. This elaborate, plasmid-encoded system involves an expression site that can acquire either variable large protein (vlp) or variable small. . . homology sequences (DHS) found periodically among the vlp/vsp archival genes. Previous studies have shown that antigenic variation in relapsing fever ***Borrelia*** not only permits the evasion of host antibody responses, but can also result in changes in neurotropism and other pathogenic. . . relapsing fever vlp genes, has evolved a completely different antigenic variation mechanism involving segmental recombination from a contiguous array of ***vls*** silent

cassettes. These two systems thus appear to represent divergence from a common precursor followed by functional convergence to create. . .
BT Spirochaetaceae; Spirochaetales; Gracilicutes; bacteria; prokaryotes; ***Borrelia***
ORGN ***Borrelia*** ; ***Borrelia*** hermsii

L4 ANSWER 9 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 6
AN 2006:406251 BIOSIS <<LOGINID::20090609>>
DN PREV200600407284
TI Immunodominant epitope in the C-terminus of a variable major protein in ***Borrelia*** duttonii, an agent of tick-borne relapsing fever.
AU Tabuchi, Norihiko [Reprint Author]; Tomoda, Koichiro; Kawaguchi, Hiroshi; Iwamoto, Hiroyuki; Fukunaga, Masahito
CS Fukuyama Univ, Fac Pharm and Pharmaceut Sci, Mol Microbiol Lab, Gakuencho 1, Hiroshima 7290292, Japan
tabuchi@fupharm.fukuyama-u.ac.jp
SO Microbiology and Immunology, (2006) Vol. 50, No. 4, pp. 293-305.
CODEN: MIIMDV. ISSN: 0385-5600.
DT Article
LA English
ED Entered STN: 17 Aug 2006
Last Updated on STN: 17 Aug 2006
AB ***Borrelia*** duttonii strain Ly was isolated from a child with tick-borne relapsing fever in Tanzania. B. duttonii produces variable major proteins (***Vmps***), which undergo antigenic variation. We previously reported transcription of the ***vmpP*** gene, which is one of the ***Vmp*** genes in strain Ly, detected in vitro cultivation. In the current study, we purified the recombinant non-lipidated ***VmpP*** protein by affinity chromatography and produced ***VmpP*** polyclonal antibodies. Antigenicity of ***VmpP*** was examined by Western immunoblot analysis and peptide-based enzyme-linked immunosorbent assays. Antigenic epitopes were shown to comprise five regions interspersed within the ***VmpP*** primary amino acid sequence. Synthetic peptides spanning residues of three of five regions, 232-237 (LASIVD), 280-285 (AGGIAL), and 350-355 (KAADQQ), reacted strongly with the ***VmpP*** -specific antibody and these residues were identified as epitopes. In particular, the C-terminal domain (KAADQQ) of this protein was immunoreactive. Further research based on our results will promote the development of a recombinant vaccine for B. duttonii infection.
TI Immunodominant epitope in the C-terminus of a variable major protein in ***Borrelia*** duttonii, an agent of tick-borne relapsing fever.
AB ***Borrelia*** duttonii strain Ly was isolated from a child with tick-borne relapsing fever in Tanzania. B. duttonii produces variable major proteins (***Vmps***), which undergo antigenic variation. We previously reported transcription of the ***vmpP*** gene, which is one of the ***Vmp*** genes in strain Ly, detected in vitro cultivation. In the current study, we purified the recombinant non-lipidated ***VmpP*** protein by affinity chromatography and produced ***VmpP*** polyclonal antibodies. Antigenicity of ***VmpP*** was examined by Western immunoblot analysis and peptide-based enzyme-linked immunosorbent assays. Antigenic epitopes were shown to comprise five regions interspersed within the ***VmpP*** primary amino acid sequence. Synthetic peptides spanning residues of three of five regions, 232-237 (LASIVD), 280-285 (AGGIAL), and 350-355 (KAADQQ), reacted strongly with the ***VmpP*** -specific antibody and these residues were identified as epitopes. In particular, the C-terminal domain (KAADQQ) of this protein

was immunoreactive. Further. . .
ORGN . . .
Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia duttonii (species): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***Borrelia*** duttonii ***vmpP*** gene gene (Spirochaetaceae)

L4 ANSWER 10 OF 87 MEDLINE on STN DUPLICATE 7
AN 2006527807 MEDLINE <<LOGINID::20090609>>
DN PubMed ID: 16914037
TI Comparative genome analysis: selection pressure on the ***Borrelia*** ***vls*** cassettes is essential for infectivity.
AU Glockner Gernot; Schulte-Spechtel Ulrike; Schilhabel Markus; Felder Marius; Suhnel Jurgen; Wilske Bettina; Platzer Matthias
CS Genome Analysis Group, Leibniz Institute for Age Research - Fritz Lipmann Institute, Beutenbergstr, 11, 07745 Jena, Germany.. gernot@fli-leibniz.de
SO BMC genomics, (2006) Vol. 7, pp. 211. Electronic Publication: 2006-08-16.
Journal code: 100965258. E-ISSN: 1471-2164.
Report No.: NLM-PMC1559707.
CY England: United Kingdom
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200610
ED Entered STN: 6 Sep 2006
Last Updated on STN: 19 Oct 2006
Entered Medline: 18 Oct 2006
AB BACKGROUND: At least three species of ***Borrelia*** burgdorferi sensu lato (Bbsl) cause tick-borne Lyme disease. Previous work including the genome analysis of B. burgdorferi B31 and B. garinii PBi suggested a highly variable plasmid part. The frequent occurrence of duplicated sequence stretches, the observed plasmid redundancy, as well as the mainly unknown function and variability of plasmid encoded genes rendered the relationships between plasmids within and between species largely unresolvable. RESULTS: To gain further insight into ***Borreliae*** genome properties we completed the plasmid sequences of B. garinii PBi, added the genome of a further species, B. afzelii PKo, to our analysis, and compared for both species the genomes of pathogenic and apathogenic strains.The core of all Bbsl genomes consists of the chromosome and two plasmids collinear between all species. We also found additional groups of plasmids, which share large parts of their sequences. This makes it very likely that these plasmids are relatively stable and share common ancestors before the diversification of ***Borrelia*** species.The analysis of the differences between B. garinii PBi and B. afzelii PKo genomes of low and high passages revealed that the loss of infectivity is accompanied in both species by a loss of similar genetic material. Whereas B. garinii PBi suffered only from the break-off of a plasmid end, B. afzelii PKo lost more material, probably an entire plasmid. In both

cases the ***vls*** gene locus encoding for variable surface proteins is affected. CONCLUSION: The complete genome sequences of a B. garinii and a B. afzelii strain facilitate further comparative studies within the genus Borrellia. Our study shows that loss of infectivity can be traced back to only one single event in B. garinii PBi: the loss of the ***vls*** cassettes possibly due to error prone gene conversion. Similar albeit extended losses in B. afzelii PKo support the hypothesis that infectivity of ***Borrelia*** species depends heavily on the evasion from the host response.

TI Comparative genome analysis: selection pressure on the ***Borrelia*** ***vls*** cassettes is essential for infectivity.

AB BACKGROUND: At least three species of ***Borrelia*** burgdorferi sensu lato (Bbsl) cause tick-borne Lyme disease. Previous work including the genome analysis of B. burgdorferi B31 and B.. . . plasmid encoded genes rendered the relationships between plasmids within and between species largely unresolvable. RESULTS: To gain further insight into ***Borreliae*** genome properties we completed the plasmid sequences of B. garinii PBi, added the genome of a further species, B. afzelii. . . sequences. This makes it very likely that these plasmids are relatively stable and share common ancestors before the diversification of ***Borrelia*** species.The analysis of the differences between B. garinii PBi and B. afzelii PKo genomes of low and high passages revealed. . . the break-off of a plasmid end, B. afzelii PKo lost more material, probably an entire plasmid. In both cases the ***vls*** gene locus encoding for variable surface proteins is affected. CONCLUSION: The complete genome sequences of a B. garinii and a. . . loss of infectivity can be traced back to only one single event in B. garinii PBi: the loss of the ***vls*** cassettes possibly due to error prone gene conversion. Similar albeit extended losses in B. afzelii PKo support the hypothesis that infectivity of ***Borrelia*** species depends heavily on the evasion from the host response.

CT ****Borrelia: GE, genetics***
*** Borrelia: PY, pathogenicity***
*** Borrelia Infections: MI, microbiology***
*** Borrelia burgdorferi: GE, genetics***
*** Borrelia burgdorferi: PY, pathogenicity***
Chromosomes, Bacterial: GE, genetics
DNA, Bacterial: CH, chemistry
DNA, Bacterial: GE, genetics
Genes, Bacterial: GE, genetics

. . .

L4 ANSWER 11 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 8

AN 2006:675157 BIOSIS <<LOGINID::20090609>>

DN PREV200600667335

TI Comparative genome analysis: selection pressure on the ***Borrelia*** ***vls*** cassettes is essential for infectivity.

AU Gloeckner, Gernot [Reprint Author]; Schulte-Spechtel, Ulrike; Schilhabel, Markus; Felder, Marius; Suehnel, Juergen; Wilske, Bettina; Platzer, Matthias

CS Fritz Lipmann Inst, Leibniz Inst Age Res, Genome Anal Grp, Beutenbergstr 11, D-07745 Jena, Germany
gernot@fli-leibniz.de; Spechtel@m3401.mpk.med.uni-muenchen.de; mbs@fli-leibniz.de; mfelder@fli-leibniz.de; jsuehnel@fli-leibniz.de; Bettina.Wilske@mvp-bak.med.uni-muenchen.de; mplatzer@fli-leibniz.de

SO BMC Genomics, (AUG 16 2006) Vol. 7, pp. Article No.: 211.

ISSN: 1471-2164.
DT Article
LA English
OS genBank-CP000397CP000406
ED Entered STN: 6 Dec 2006
Last Updated on STN: 20 Sep 2007
AB Background: At least three species of ***Borrelia*** burgdorferi sensu lato (Bbsl) cause tick-borne Lyme disease. Previous work including the genome analysis of B. burgdorferi B31 and B. garinii PBi suggested a highly variable plasmid part. The frequent occurrence of duplicated sequence stretches, the observed plasmid redundancy, as well as the mainly unknown function and variability of plasmid encoded genes rendered the relationships between plasmids within and between species largely unresolvable.Results: To gain further insight into ***Borreliae*** genome properties we completed the plasmid sequences of B. garinii PBi, added the genome of a further species, B. afzelii PKo, to our analysis, and compared for both species the genomes of pathogenic and apathogenic strains.The core of all Bbsl genomes consists of the chromosome and two plasmids collinear between all species. We also found additional groups of plasmids, which share large parts of their sequences. This makes it very likely that these plasmids are relatively stable and share common ancestors before the diversification of ***Borrelia*** species.The analysis of the differences between B. garinii PBi and B. afzelii PKo genomes of low and high passages revealed that the loss of infectivity is accompanied in both species by a loss of similar genetic material. Whereas B. garinii PBi suffered only from the break-off of a plasmid end, B. afzelii PKo lost more material, probably an entire plasmid. In both cases the ***vls*** gene locus encoding for variable surface proteins is affected.Conclusion: The complete genome sequences of a B. garinii and a B. afzelii strain facilitate further comparative studies within the genus Borrellia. Our study shows that loss of infectivity can be traced back to only one single event in B. garinii PBi: the loss of the ***vls*** cassettes possibly due to error prone gene conversion. Similar albeit extended losses in B. afzelii PKo support the hypothesis that infectivity of ***Borrelia*** species depends heavily on the evasion from the host response.
TI Comparative genome analysis: selection pressure on the ***Borrelia*** ***vls*** cassettes is essential for infectivity.
AB Background: At least three species of ***Borrelia*** burgdorferi sensu lato (Bbsl) cause tick-borne Lyme disease. Previous work including the genome analysis of B. burgdorferi B31 and B.. . . of plasmid encoded genes rendered the relationships between plasmids within and between species largely unresolvable.Results: To gain further insight into ***Borreliae*** genome properties we completed the plasmid sequences of B. garinii PBi, added the genome of a further species, B. afzelii. . . sequences. This makes it very likely that these plasmids are relatively stable and share common ancestors before the diversification of ***Borrelia*** species.The analysis of the differences between B. garinii PBi and B. afzelii PKo genomes of low and high passages revealed. . . the break-off of a plasmid end, B. afzelii PKo lost more material, probably an entire plasmid. In both cases the ***vls*** gene locus encoding for variable surface proteins is affected.Conclusion: The complete genome sequences of a B. garinii and a B.. . . loss of infectivity can be traced back to only one single event in B. garinii PBi: the loss of the ***vls*** cassettes possibly due to error prone gene conversion. Similar albeit extended losses in B. afzelii PKo support the hypothesis that infectivity of ***Borrelia*** species depends heavily

on the evasion from the host response.
ORGN . . .
Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi (species): pathogen, strain-B31
Borrelia garinii (species): pathogen, strain-PBi
Borrelia afzelii (species): pathogen, strain-PKo
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 12 OF 87 CABA COPYRIGHT 2009 CABI on STN DUPLICATE 9
AN 2007:2067 CABA <<LOGINID::20090609>>
DN 20063185553
TI Comparative genome analysis: selection pressure on the ***Borrelia*** ***vls*** cassettes is essential for infectivity
AU Glockner, G.; Schulte-Spechtel, U.; Schilhabel, M.; Felder, M.; Suhnel, J.; Wilske, B.; Platzer, M.
CS Genome Analysis Group, Leibniz Institute for Age Research-Fritz Lipmann Institute, Beutenbergstr. 11, 07745 Jena, Germany. gernot@fli-leibniz.de; Spechtel@m3401.mpk.med.uni-muenchen.de; mbs@fli-leibniz.de; mfelder@fli-leibniz.de; jsuehnel@fli-leibniz.de; Bettina.Wilske@mvp-bak.med.uni-muenchen.de; mplatzer@fli-leibniz.de
SO BMC Genomics, (2006) Vol. 7, No. 211, pp. (16 August 2006). 36 ref.
Publisher: BioMed Central Ltd. London
ISSN: 1471-2164
URL: http://www.biomedcentral.com/content/pdf/1471-2164-7-211.pdf
CY United Kingdom
DT Journal
LA English
ED Entered STN: 8 Jan 2007
Last Updated on STN: 8 Jan 2007
AB Background: At least 3 species of ***Borrelia*** burgdorferi sensu lato (Bbsl) cause tickborne Lyme disease. Previous work, including the genome analysis of B. burgdorferi B31 and B. garinii PBi, suggested a highly variable plasmid part. The frequent occurrence of duplicated sequence stretches, the observed plasmid redundancy, as well as the mainly unknown function and variability of plasmid encoded genes render the relationships between plasmids within and between species largely unresolvable. Results: To gain further insight into the ***Borrelia*** genome properties, the plasmid sequences of B. garinii PBi were completed, the genome of B. afzelii PKo was analysed, and the genomes of the pathogenic and apathogenic strains of both species were compared. The core of all Bbsl genomes consisted of the chromosome and 2 plasmids collinear between all species. Additional groups of plasmids, which share large parts of their sequences, were observed, suggesting that these plasmids are relatively stable and share common ancestors before the diversification of ***Borrelia*** species. The analysis of the differences between B. garinii PBi and B. afzelii PKo genomes of low and high passages revealed that the loss of infectivity was accompanied in both species by a loss of similar genetic material. B. garinii PBi suffered only from the break-off of a plasmid end, whereas B. afzelii PKo lost more material, probably an entire plasmid. In both cases, the

vls gene locus encoding for variable surface proteins was affected. Conclusion: The complete genome sequences of a B. garinii and a B. afzelii strain facilitate further comparative studies within the genus ***Borrelia*** . The loss of infectivity can be traced back to only one single event in B. garinii PBi: the loss of the ***vls*** cassettes is possibly due to error prone gene conversion. Similar albeit extended losses in B. afzelii PKo support the hypothesis that the infectivity of ***Borrelia*** species depends heavily on the evasion from the host response.

TI Comparative genome analysis: selection pressure on the ***Borrelia*** ***vls*** cassettes is essential for infectivity.

AB Background: At least 3 species of ***Borrelia*** burgdorferi sensu lato (Bbsl) cause tickborne Lyme disease. Previous work, including the genome analysis of B. burgdorferi B31 and B.. . . encoded genes render the relationships between plasmids within and between species largely unresolvable. Results: To gain further insight into the ***Borrelia*** genome properties, the plasmid sequences of B. garinii PBi were completed, the genome of B. afzelii PKo was analysed, and. . . of their sequences, were observed, suggesting that these plasmids are relatively stable and share common ancestors before the diversification of ***Borrelia*** species. The analysis of the differences between B. garinii PBi and B. afzelii PKo genomes of low and high passages. . . break-off of a plasmid end, whereas B. afzelii PKo lost more material, probably an entire plasmid. In both cases, the ***vls*** gene locus encoding for variable surface proteins was affected. Conclusion: The complete genome sequences of a B. garinii and a B. afzelii strain facilitate further comparative studies within the genus ***Borrelia*** . The loss of infectivity can be traced back to only one single event in B. garinii PBi: the loss of the ***vls*** cassettes is possibly due to error prone gene conversion. Similar albeit extended losses in B. afzelii PKo support the hypothesis that the infectivity of ***Borrelia*** species depends heavily on the evasion from the host response.

BT ***Borrelia*** ; Spirochaetaceae; Spirochaetales; Gracilicutes; bacteria; prokaryotes

ORGN ***Borrelia*** afzelii; ***Borrelia*** burgdorferi; ***Borrelia*** garinii

L4 ANSWER 13 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2006:134820 BIOSIS <<LOGINID::20090609>>

DN PREV200600145254

TI ***Vmp*** -like sequences of pathogenic ***Borrelia*** .

AU Norris, Steven J. [Inventor]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]

CS Houston, TX USA

ASSIGNEE: Board of Regents, The University of Texas System

PI US 06878816 20050412

SO Official Gazette of the United States Patent and Trademark Office Patents, (APR 12 2005)

CODEN: OGUPE7. ISSN: 0098-1133.

DT Patent

LA English

ED Entered STN: 22 Feb 2006

Last Updated on STN: 22 Feb 2006

AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA

sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.

TI ***Vmp*** -like sequences of pathogenic ***Borrelia*** .

AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .

IT . . .
Clinical Immunology (Human Medicine, Medical Sciences); Infection; Clinical Chemistry (Allied Medical Sciences); Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Diseases
Borrelia infection: bacterial disease, drug therapy, prevention and control

IT Chemicals & Biochemicals
DNA sequences; ***Vmp*** -like sequences; ***Borrelia*** polypeptide antigens: diagnostic-drug, immunostimulant-drug, immunologic-drug

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia (genus): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 14 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 10

AN 2005:554633 BIOSIS <<LOGINID::20090609>>

DN PREV200510340099

TI Variable tick protein in two genomic groups of the relapsing fever spirochete ***Borrelia*** hermsii in western North America.

AU Porcella, Stephen F.; Raffel, Sandra J.; Anderson, Donald E. Jr; Gilk, Stacey D.; Bono, James L.; Schrumpf, Merry E.; Schwan, Tom G. [Reprint Author]

CS NIAID, Rocky Mt Labs, Lab Human Bacterial Pathogenesis, 903 S 4th St, Hamilton, MT 59840 USA
tom_schwan@nih.gov

SO Infection and Immunity, (OCT 2005) Vol. 73, No. 10, pp. 6647-6658. CODEN: INFIBR. ISSN: 0019-9567.

DT Article

LA English

ED Entered STN: 7 Dec 2005
Last Updated on STN: 7 Dec 2005

AB ***Borrelia*** hermsii is the primary cause of tick-borne relapsing fever in North America. When its tick vector, Ornithodoros hermsi, acquires these spirochetes from the blood of an infected mammal, the bacteria switch their outer surface from one of,many bloodstream variable major proteins (***Vmps***) to a unique protein, Vtp (Vsp33). Vtp may be critical for successful tick transmission of B. hermsii; however, the

gene encoding this protein has been described previously in only one isolate. Here we identified and sequenced the vtp gene in 31 isolates of B. hermsii collected over 40 years from localities throughout much of its known geographic distribution. Seven major Vtp types were found. Little or no sequence variation existed within types, but between them significant variation was observed,, similar to the pattern of diversity described for the outer surface protein C (OspC) gene in Lyme disease spirochetes. The pattern of sequence relatedness among the Vtp types was incongruent in two branches compared to two genomic groups identified among the isolates by multilocus sequence typing of the 16S rRNA,flaB, gyrB, and glpQ genes. Therefore, both horizontal transfer and recombination within and between the two genomic, groups were responsible for some of the variation observed in the vtp gene. O. hermsi ticks were capable of transmitting spirochetes in the newly identified genomic group. Therefore, given the longevity of the tick vector and persistent infection of spirochetes in ticks, these arthropods rather than mammals may be the likely host where the exchange of spirochetal DNA occurs.

TI Variable tick protein in two genomic groups of the relapsing fever spirochete ***Borrelia*** hermsii in western North America.

AB ***Borrelia*** hermsii is the primary cause of tick-borne relapsing fever in North America. When its tick vector, Ornithodoros hermsi, acquires these. . . from the blood of an infected mammal, the bacteria switch their outer surface from one of,many bloodstream variable major proteins (***Vmps***) to a unique protein, Vtp (Vsp33). Vtp may be critical for successful tick transmission of B. hermsii; however, the gene. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia hermsii (species): pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Borrelia*** hermsii vtp gene (Spirochaetaceae); ***Borrelia*** hermsii flaB gene (Spirochaetaceae); ***Borrelia*** hermsii gyrB gene (Spirochaetaceae); ***Borrelia*** hermsii glpQ gene (Spirochaetaceae)

L4 ANSWER 15 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2004:283015 BIOSIS <<LOGINID::20090609>>

DN PREV200400283530

TI ***VMP*** -like sequences of pathogenic ***borrelia*** .

AU Norris, Steven J. [Inventor, Reprint Author]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]

CS ASSIGNEE: Board of Regents, The University of Texas System

PI US 6740744 20040525

SO Official Gazette of the United States Patent and Trademark Office Patents, (May 25 2004) Vol. 1282, No. 4.
http://www.uspto.gov/web/menu/patdata.html. e-file.
ISSN: 0098-1133 (ISSN print).

DT Patent

LA English

ED Entered STN: 9 Jun 2004

Last Updated on STN: 9 Jun 2004

AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.

TI ***VMP*** -like sequences of pathogenic ***borrelia*** .

AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .

IT Major Concepts
Equipment Apparatus Devices and Instrumentation; Infection; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Diseases
Borrelia infection: bacterial disease
Borrelia Infections (MeSH)

IT Diseases
Lyme disease: bacterial disease, diagnosis
Lyme Disease (MeSH)

IT Diseases
relapsing fever: bacterial disease, diagnosis
Relapsing Fever (MeSH)

IT Chemicals & Biochemicals
Vmp -like polypeptides: encoding DNA sequences, encoding amino
acid sequences; antibodies

IT Methods & Equipment
Borrelia infection assay method: bioassay techniques, laboratory techniques; immunodiagnosis: immunologic techniques, laboratory techniques; immunoprophylaxis: immunologic techniques, laboratory techniques; immunotherapy: clinical techniques,. . .

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia (genus): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 16 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2004:257493 BIOSIS <<LOGINID::20090609>>

DN PREV200400257602

TI ***VMP*** -like sequences of pathogenic ***Borrelia*** .

AU Norris, Steven J. [Inventor, Reprint Author]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]

CS Delmar, NY, USA
ASSIGNEE: Board of Regents, The University of Texas System

PI US 6719983 20040413

SO Official Gazette of the United States Patent and Trademark Office Patents, (Apr 13 2004) Vol. 1281, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DT Patent
LA English
ED Entered STN: 12 May 2004
Last Updated on STN: 12 May 2004
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
TI ***VMP*** -like sequences of pathogenic ***Borrelia*** .
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
IT Major Concepts
Medical Genetics (Allied Medical Sciences); Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
Borrelia ***VMP*** -like DNA sequences

L4 ANSWER 17 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:1033546 CAPLUS <<LOGINID::20090609>>
DN 142:22291
TI Nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody preparation techniques
IN Sykes, Kathryn F.; Hale, Katherine S.; Johnston, Stephen A.
PA Macrogenics, Inc., USA; Board of Regents, the University of Texas System
SO PCT Int. Appl., 121 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004103269	A2	20041202	WO 2003-US33056	20031017
WO 2004103269	A3	20051229		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2003304145	A1	20041213	AU 2003-304145	20031017
US 20050058661	A1	20050317	US 2003-688058	20031017

PRAI US 2002-419401P P 20021018
WO 2003-US33056 W 20031017
AB The invention relates to 34 antigens and nucleic acids encoding such antigens obtainable by screening a ***Borrelia*** genome, in particular a B. burgdorferi genome. In more specific aspects, the invention relates to methods of isolating such antigens and nucleic acids and to methods of using such isolated antigens for producing immune responses. The ability of an antigen to produce an immune response may be employed in vaccination or antibody prepn. techniques.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody preparation techniques
AB The invention relates to 34 antigens and nucleic acids encoding such antigens obtainable by screening a ***Borrelia*** genome, in particular a B. burgdorferi genome. In more specific aspects, the invention relates to methods of isolating such antigens. . .
SYSTEM LIMIT EXCEEDED DURING KWIC/STRING SEARCH
ST antigen gene sequence ***Borrelia*** vaccine antibody
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0043; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0043; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0072; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0133; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0351; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0451; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0508; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic

use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0540; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BB0656; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBA04; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBB14; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBE02; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBF05; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBF13; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBG24; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBJ12; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBM10; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBM11; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBO11; nucleic acid and/or polypeptide sequences of ***Borrelia***

burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBO29; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBR01; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBS36; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(BBT01; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(CP32-7; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Translation elongation factors
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(EF-G; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(GTP-binding; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(PGK; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Antigens
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(S2; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(Vls8; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(Vls9; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic

use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(VlsE1; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Transport proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(chromate-transporting; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(cp26; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(cp32-3; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(cp32-4; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(cp32-6; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(cp32-7; nucleic acid and/or polypeptide sequences of ***Borrelia***
burgdorferi for vaccination and antibody prepn. techniques)
IT Herpesviridae
(detection of; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BB0043; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BB007224; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BB0072; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BB0133; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BB0351; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn.

techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BB0451; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBB14; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBE02; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBF05; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBF13; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBG24; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBJ12; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBM10; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBM11; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic

use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBO11; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBO29; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBR01; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBS36; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gene BBT01; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(glpK; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gluA; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Transport proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(glycine/betaine/proline-binding; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(gpsA; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Antibodies and Immunoglobulins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(humanized; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Plasmids
(lp25; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Plasmids
Plasmids
Plasmids
(lp28-1; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(lp28-2; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(lp38; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(lp54; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(lp56; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Plasmids
(lp5; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(mfd; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(mutL; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Aptamers
Borrelia
Borrelia burgdorferi
DNA sequences
Immunoassay
Lyme disease
Molecular cloning
Protein sequences
Vaccines
(nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Antibodies and Immunoglobulins
RL: ANT (Analyte); ARG (Analytical reagent use); BPN (Biosynthetic preparation); DGN (Diagnostic use); NUU (Other use, unclassified); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Antigens
Gene, microbial
Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(proX; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(rho; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Proteins
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(transcription-repair coupling factor; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(trxB; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Immunization
(vaccination; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(vls8; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT Gene, microbial
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(vlsE1; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT 800367-85-5P 800367-86-6P 800367-87-7P 800926-61-8P, Protein (plasmid lp56 fragment) 800926-63-0P, Protein (plasmid cp32-4 gene BBR01) 800926-65-2P 800926-67-4P 800926-69-6P 800926-71-0P 800926-73-2P 800926-75-4P, Protein (plasmid lp25 gene BBE02) 800926-77-6P 800926-79-8P, Protein (plasmid cp32-7 gene BBO11) 800926-81-2P 800926-83-4P, Protein (plasmid lp28-1 gene BBF13) 800926-85-6P 800926-87-8P 800926-89-0P 800926-91-4P 800926-93-6P 800926-95-8P 800926-97-0P 800926-99-2P, Protein (plasmid cp32-7 gene BBO29) 800927-02-0P 800927-04-2P 800927-06-4P 800927-08-6P 800927-10-0P, Protein (plasmid lp28-2 gene BBG24) 800927-12-2P 800927-14-4P 800927-16-6P 800927-18-8P 800927-20-2P 800927-22-4P, Protein (plasmid cp32-6 gene BBM11) 800927-24-6P 800927-26-8P 800927-28-0P 800927-30-4P, Protein (plasmid lp28-1 gene BBF05) 800927-32-6P 800927-34-8P, Protein (plasmid cp32-6 gene BBM10) 800927-36-0P 800927-38-2P, Protein (plasmid cp32-3 gene BBS36) 800927-40-6P 800927-42-8P 800927-44-0P 800927-46-2P 800927-48-4P 800927-50-8P 800927-52-0P 800927-54-2P 800927-56-4P 800927-58-6P 800927-60-0P, Protein (plasmid cp26 gene BBB14) 800927-62-2P 800927-64-4P 800927-66-6P 800927-68-8P 800927-70-2P 800927-73-5P, Protein (plasmid lp28-1 gene vlsE1) 800927-75-7P 800927-77-9P 800927-79-1P 800927-82-6P 800927-84-8P 800927-86-0P, Protein

(plasmid lp5 gene BBT01) 800927-89-3P 800927-91-7P 800927-93-9P
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT 182909-40-6, GenBank U43414 200798-27-2, GenBank AE000793 200798-28-3, GenBank AE000785 200798-31-8, GenBank AE000784 200798-32-9, GenBank AE000789 200798-33-0, GenBank AE000788 200798-34-1, GenBank AE000787 200798-42-1, GenBank AE000794 247563-25-3, GenBank AE001575 247563-26-4, GenBank AE001576 247563-27-5, GenBank AE001577 247563-28-6, GenBank AE001578 247563-29-7, GenBank AE001579 247563-30-0, GenBank AE001580 247563-31-1, GenBank AE001581 247563-32-2, GenBank AE001582 247563-33-3, GenBank AE001584 254953-60-1, GenBank AF169008
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. technique)

IT 9001-83-6P, Phosphoglycerate kinase 9030-66-4P, Glycerol kinase 9074-14-0P, Thioredoxin reductase 9075-65-4P, Glycerol-3-phosphate dehydrogenase 9076-84-0P, Coproporphyrinogen III oxidase 295324-05-9P, Glutamyl-tRNA amidotransferase
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

IT 800926-60-7P, DNA (plasmid lp56 gene fragment) 800926-62-9P, DNA (plasmid cp32-4 gene BBR01) 800926-64-1P 800926-66-3P 800926-68-5P 800926-70-9P 800926-72-1P, DNA (plasmid lp25 gene BBE02 fragment) 800926-74-3P, DNA (plasmid lp25 gene BBE02) 800926-76-5P, DNA (plasmid cp32-7 gene BBO11 fragment) 800926-78-7P, DNA (plasmid cp32-7 gene BBO11) 800926-80-1P
800926-82-3P, DNA (plasmid lp28-1 gene BBF13) 800926-84-5P 800926-86-7P 800926-88-9P 800926-90-3P 800926-92-5P 800926-94-7P 800926-96-9P, DNA (plasmid cp32-7 gene BBO29 fragment) 800926-98-1P, DNA (plasmid cp32-7 gene BBO29) 800927-00-8P, DNA (plasmid lp38 gene BBJ12 fragment) 800927-01-9P, DNA (plasmid lp38 gene BBJ12) 800927-03-1P 800927-05-3P 800927-07-5P, DNA (plasmid lp28-2 gene BBG24 fragment) 800927-09-7P, DNA (plasmid lp28-2 gene BBG24) 800927-11-1P 800927-13-3P 800927-15-5P 800927-17-7P 800927-19-9P, DNA (plasmid cp32-6 gene BBM11 fragment) 800927-21-3P, DNA (plasmid cp32-6 gene BBM11) 800927-23-5P 800927-25-7P 800927-27-9P, DNA (plasmid lp28-1 gene BBF05 fragment) 800927-29-1P, DNA (plasmid lp28-1 gene BBF05) 800927-31-5P, DNA (plasmid cp32-6 gene BBM10 fragment) 800927-33-7P, DNA (plasmid cp32-6 gene BBM10) 800927-35-9P, DNA (plasmid cp32-3 gene BBS36 fragment) 800927-37-1P, DNA (plasmid cp32-3 gene BBS36) 800927-39-3P 800927-41-7P 800927-43-9P 800927-45-1P 800927-47-3P 800927-49-5P, DNA (plasmid lp54 gene BBA04 fragment) 800927-51-9P, DNA (plasmid lp54 gene BBA04) 800927-53-1P 800927-55-3P 800927-57-5P, DNA (plasmid cp26 gene BBB14 fragment) 800927-59-7P, DNA (plasmid cp26 gene BBB14) 800927-61-1P 800927-63-3P 800927-65-5P, DNA (plasmid lp28-1 gene ***vls*** fragment) 800927-67-7P, DNA (plasmid lp28-1 gene vls8 fragment) 800927-69-9P, DNA (plasmid lp28-1 gene vls9 fragment) 800927-71-3P 800927-72-4P, DNA (plasmid lp28-1 gene vlpE1) 800927-74-6P 800927-76-8P 800927-78-0P 800927-80-4P 800927-81-5P 800927-83-7P, DNA (plasmid lp5 gene BBT01 fragment) 800927-85-9P, DNA

(plasmid lp5 gene BBT01) 800927-87-1P 800927-88-2P 800927-90-6P 800927-92-8P
RL: BPN (Biosynthetic preparation); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleotide sequence; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)
IT 800932-74-5 800932-75-6
RL: PRP (Properties)
(unclaimed nucleotide sequence; nucleic acid and/or polypeptide sequences of ***Borrelia*** burgdorferi for vaccination and antibody prepn. techniques)

L4 ANSWER 18 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2004:565053 CAPLUS <<LOGINID::20090609>>
DN 141:118336
TI Polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease
IN Norris, Steven J.
PA Board of Regents, University of Texas System, USA
SO PCT Int. Appl., 182 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004058181	A2	20040715	WO 2003-US41182	20031222
WO 2004058181	A3	20050421		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
AU 2003299872	A1	20040722	AU 2003-299872	20031222
EP 1572714	A2	20050914	EP 2003-800145	20031222
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
US 20060240035	A1	20061026	US 2005-539956	20050617
PRAI US 2002-435077P	P	20021220		
WO 2003-US41182	W	20031222		

AB The invention claims DNA sequences encoding variable major protein (***VMP***)-like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the prodn. of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. The invention also claims use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments, and antibodies. Examples of the invention show reactivity of

human Lyme disease serum with recombinant ***Borrelia*** afzelii ***Vls*** (variable major protein-like sequence) protein ***VLS*** -BA13 and with recombinant B. garinii ***Vls*** protein ***VLS*** -BG10. Mouse anti- ***Borrelia*** burgdorferi serum also reacted in an enzyme immunoassay with the recombinant proteins ***VLS*** -BA13 and ***VLS*** -BG10. The examples also show gene organization of ***vls*** silent cassette loci from B. afzelii strain ACAI and B. garinii strain Ip90, expression of gene vlsE, and cDNA sequences of vlsE variants cloned from strains that were passaged through mice.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI Polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease

AB The invention claims DNA sequences encoding variable major protein (***VMP***)-like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . . the described polypeptides, DNA segments, and antibodies. Examples of the invention show reactivity of human Lyme disease serum with recombinant ***Borrelia*** afzelii ***Vls*** (variable major protein-like sequence) protein ***VLS*** -BA13 and with recombinant B. garinii ***Vls*** protein ***VLS*** -BG10. Mouse anti- ***Borrelia*** burgdorferi serum also reacted in an enzyme immunoassay with the recombinant proteins ***VLS*** -BA13 and ***VLS*** -BG10. The examples also show gene organization of ***vls*** silent cassette loci from B. afzelii strain ACAI and B. garinii strain Ip90, expression of gene vlsE, and cDNA sequences. . .

ST DNA sequence ***Borrelia*** gene ***vls*** antigen; ***Borrelia*** gene ***vls*** diagnosis vaccine immunotherapy Lyme disease infection

IT Infection
(bacterial; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Immunoassay
(enzyme-linked immunosorbent assay; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Recombination, genetic
(gene conversion; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

IT Diagnosis
(immunodiagnosis; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

IT Animals
Bos taurus
Canis familiaris
Cervidae
Equus caballus
Human

Mus
(infection; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Antibodies and Immunoglobulins
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(labeled; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Antibodies and Immunoglobulins
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(monoclonal; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Antigenic variation
Blood analysis
Borrelia afzelii
Borrelia burgdorferi
Borrelia garinii
DNA sequences
Genetic polymorphism
Immunity
Immunoassay
Immunoblotting
Immunoprecipitation
Immunotherapy
Lyme disease
Molecular cloning
Nucleic acid amplification (method)
Plasmids
Protein sequences
Radioimmunoassay
Test kits
Urine analysis
cDNA sequences
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Antigens
RL: ANT (Analyte); BPN (Biosynthetic preparation); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Nucleic acids
RNA
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT Antibodies and Immunoglobulins

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Escherichia coli
(recombinant host; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

IT Fever and Hyperthermia
(relapsing; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Repetitive DNA
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***vls*** silent cassettes; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***vls*** ; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

IT Gene, microbial
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(vlsE; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721865-74-3 721865-75-4 721865-91-4 721865-92-5
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** afzelii strain ACAI gene vls13 primer; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721865-72-1
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** burgdorferi B31 vlsE and ***vls*** silent

cassette flanking direct repeat; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721865-93-6 721865-94-7 721865-95-8 721865-96-9
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** garinii strain Ip90 gene vls10 primer; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-14-5
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4470; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-15-6
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4471; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-03-2
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4540; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-11-2
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4545; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-10-1
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4548; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-12-3
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(***Borrelia*** gene ***vls*** specific primer 4587;

polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721863-13-4

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(***Borrelia*** gene ***vls*** specific primer 4588; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)

IT 721862-92-6P 721862-95-9P 721863-00-9P 721863-01-0P 721863-02-1P
721863-07-6P 721863-08-7P 721863-09-8P 721863-19-0P 721863-20-3P
721863-33-8P 721863-34-9P 721863-35-0P 721863-36-1P 721863-37-2P
721863-38-3P 721863-39-4P 721863-40-7P 721863-41-8P 721863-42-9P
721863-43-0P 721863-45-2P 721863-48-5P 721863-62-3P 721863-63-4P
721863-64-5P 721863-65-6P 721863-66-7P 721863-67-8P 721863-68-9P
721863-70-3P 721863-73-6P 721863-74-7P 721865-61-8P, Antigen (plasmid pBG-10-1 gene vls10) 721865-63-0P 721865-64-1P 721865-65-2P
721865-66-3P 721865-67-4P 721865-68-5P 721865-71-0P, Antigen (plasmid pBA-13-1 gene vls13)

RL: ANT (Analyte); BPN (Biosynthetic preparation); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)

(amino acid sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

IT 511612-64-9 511612-65-0 511612-66-1 511612-67-2 511612-68-3
511612-69-4 511612-70-7 511612-71-8 511612-72-9 511612-73-0
511612-74-1 511612-75-2 511612-76-3 511612-77-4 511612-78-5
511612-79-6, Antigen (***Borrelia*** afzelii strain ACAI clone 2622 gene vlsE C-terminal fragment) 511612-80-9, Antigen (***Borrelia*** afzelii strain ACAI clone 2624a gene vlsE C-terminal fragment)
511612-81-0, Antigen (***Borrelia*** afzelii strain ACAI clone 2624b gene vlsE C-terminal fragment) 511612-82-1, Antigen (***Borrelia*** afzelii strain ACAI clone 2625 gene vlsE fragment) 511612-83-2
511612-84-3 511612-85-4 511612-86-5 511612-87-6 511612-88-7
511612-89-8 511612-90-1 511612-91-2 511612-92-3 511612-93-4
511612-94-5 511612-95-6 511612-96-7, Antigen (***Borrelia*** garinii strain Ip90 clone 17 gene vlsE fragment) 511612-97-8, Antigen (***Borrelia*** garinii strain Ip90 clone 20 gene vlsE fragment)
511612-98-9, Antigen (***Borrelia*** garinii strain Ip90 clone 21 gene vlsE fragment) 511612-99-0, Antigen (***Borrelia*** garinii strain Ip90 clone 23 gene vlsE fragment)

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

IT 721862-91-5 721862-96-0 721862-97-1 721862-98-2 721862-99-3
721863-04-3 721863-05-4 721863-06-5 721863-16-7 721863-21-4
721863-22-5 721863-23-6 721863-24-7 721863-25-8 721863-26-9
721863-27-0 721863-28-1 721863-29-2 721863-30-5 721863-31-6
721863-32-7 721863-44-1 721863-46-3 721863-47-4 721863-49-6
721863-50-9 721863-51-0 721863-52-1 721863-53-2 721863-54-3

721863-55-4 721863-56-5 721863-57-6 721863-58-7 721863-59-8
721863-60-1 721863-61-2 721863-69-0 721863-71-4 721863-72-5
721865-60-7, DNA (plasmid pBG-10-1 gene vls10) 721865-62-9, DNA (plasmid pBA-13-1 gene vls13) 721865-69-6 721865-70-9
RL: ANT (Analyte); BUU (Biological use, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)
IT 503713-49-3 503713-50-6 503713-51-7 503713-52-8 503713-53-9
503713-54-0 503713-55-1 503713-56-2 503713-57-3 503713-58-4
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)
IT 58-85-5D, Biotin, conjugates
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT 145856-09-3, GenBank L04788 391840-97-4, GenBank U76405
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT 721865-73-2
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(restriction endonuclease EcoRI-site linker; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT 721869-20-1 721869-22-3 721869-24-5
RL: PRP (Properties)
(unclaimed nucleotide sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT 721869-21-2 721869-23-4
RL: PRP (Properties)
(unclaimed protein sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic and therapeutic uses against infection and Lyme disease)
IT 116934-33-9
RL: PRP (Properties)
(unclaimed sequence; polynucleotide and polypeptide sequences for ***vls*** genes of pathogenic ***Borrelia*** and their diagnostic
and therapeutic uses against infection and Lyme disease)

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AN 2005:50985 BIOSIS <<LOGINID::20090609>>

DN PREV200500047406

TI Effects of vlsE complementation on the infectivity of ***Borrelia*** burgdorferi lacking the linear plasmid lp28-1.

AU Lawrenz, Matthew B.; Wooten, R. Mark; Norris, Steven J. [Reprint Author]

CS Sch MedDept Pathol and Lab Med, Univ Texas, POB 20708, Houston, TX, 77225, USA
steven.j.norris@uth.tmc.edu

SO Infection and Immunity, (November 2004) Vol. 72, No. 11, pp. 6577-6585. print.
ISSN: 0019-9567 (ISSN print).

DT Article

LA English

ED Entered STN: 26 Jan 2005
Last Updated on STN: 26 Jan 2005

AB The loss of linear plasmid lp28-1, which contains the ***vls*** antigenic variation locus, is associated with reduced infectivity of ***Borrelia*** burgdorfieri in immunocompetent mice. The recombinant shuttle vector pBBE22, which includes the virulence determinant BBE22 from lp25 and restores infectivity to readily transformable B. burgdorferi lacking lp25 and lp56, was used to determine the effect of trans expression of vlsE on virulence. Spirochetes lacking lp28-1 were complemented with the plasmid pBBE22:vlsE, containing both BBE22 and vlsE. VlsE protein produced by this construct was expressed and surface accessible in in vitro-cultured B. burgdorferi, as determined by surface proteolysis and immunoblot analysis. Clones lacking lp25 but containing lp28-1 and either pBBE22 or pBBE22:vlsE were reisolated consistently from immunocompetent mice 8 weeks after infection. In contrast, a clone lacking both lp25 and lp28-1 and complemented with pBBE22:vlsE was isolated from only a single tissue of one of six C3H/HeN mice 8 weeks postinfection. These results indicate that either an intact v/s antigenic variation locus or another determinant on lp28-1 is required to restore complete infectivity. In addition, an isogenic clone that retained lp28-1 was complemented with the v/sE shuttle plasmid and was examined for vlsE sequence variation and infectivity. Sequence variation was not observed for the shuttle plasmid, indicating that the cis arrangement of v/sE and the ***vls*** silent cassettes in lp28-1 facilitate vlsE gene conversion. Lack of vlsE sequence variation on the shuttle plasmid thus did not result in clearance of the trans-complemented strain in immunocompetent mice under the conditions tested.

TI Effects of vlsE complementation on the infectivity of ***Borrelia*** burgdorferi lacking the linear plasmid lp28-1.

AB The loss of linear plasmid lp28-1, which contains the ***vls*** antigenic variation locus, is associated with reduced infectivity of ***Borrelia*** burgdorfieri in immunocompetent mice. The recombinant shuttle vector pBBE22, which includes the virulence determinant BBE22 from lp25 and restores infectivity. . . and infectivity. Sequence variation was not observed for the shuttle plasmid, indicating that the cis arrangement of v/sE and the ***vls*** silent cassettes in lp28-1 facilitate vlsE gene conversion. Lack of vlsE sequence variation on the shuttle plasmid thus did not. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi (species): pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 20 OF 87 MEDLINE on STN
AN 2004243144 MEDLINE <<LOGINID::20090609>>
DN PubMed ID: 15128807
TI Lysine-dependent multipoint binding of the ***Borrelia*** burgdorferi virulence factor outer surface protein E to the C terminus of factor H.
AU Alitalo Antti; Meri Taru; Chen Tong; Lankinen Hilkka; Cheng Zhu-Zhu; Jokiranta T Sakari; Seppala Ilkka J T; Lahdenne Pekka; Hefty P Scott; Akins Darrin R; Meri Seppo
CS Department of Bacteriology and Immunology, Haartman Institute and Helsinki University Central Hospital, University of Helsinki, Helsinki, Finland.
NC AI-07364 (United States NIAID NIH HHS)
RR-15564 (United States NCRR NIH HHS)
SO Journal of immunology (Baltimore, Md. : 1950), (2004 May 15) Vol. 172, No. 10, pp. 6195-201.
Journal code: 2985117R. ISSN: 0022-1767.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 200409
ED Entered STN: 15 May 2004
Last Updated on STN: 3 Sep 2004
Entered Medline: 2 Sep 2004
AB Serum resistance, an important virulence determinant of ***Borrelia*** burgdorferi sensu lato strains belonging to the ***Borrelia*** afzelii and B. burgdorferi sensu stricto genotypes, is related to binding of the complement inhibitor factor H to the spirochete surface protein outer surface protein E (OspE) and its homologues. In this study, we show that the C-terminal short consensus repeats 18-20 of both human and mouse factor H bind to OspE. Analogously, factor H-related protein 1, a distinct plasma protein with three short consensus repeat domains homologous to those in factor H, bound to OspE. Deleting 15-aa residues (region V) from the C terminus of the OspE paralog P21 (a 20.7-kDa OspE-paralogous surface lipoprotein in the B. burgdorferi sensu stricto 297 strain) abolished factor H binding. However, C-terminal peptides from OspE, P21, or OspEF-related protein P alone and the C-terminal deletion mutants of P21 inhibited factor H binding to OspE only partially when compared with full-length P21 or its N-terminal mutant. Alanine substitution of amino acids in peptides from the key binding regions of the OspE family indicated that several lysine residues are required for factor H binding. Thus, the ***borrelial*** OspE family proteins bind the C inhibitor factor H via multiple sites in a lysine-dependent manner. The C-terminal site V (Ala(151)-Lys(166)) is necessary, but not sufficient, for factor H binding in both rodents and humans. Identification of the necessary binding sites forms a basis for the development of vaccines that block the factor H-OspE interaction and thereby promote the killing of ***Borreliae*** .
TI Lysine-dependent multipoint binding of the ***Borrelia*** burgdorferi

virulence factor outer surface protein E to the C terminus of factor H.
AB Serum resistance, an important virulence determinant of ***Borrelia*** burgdorferi sensu lato strains belonging to the ***Borrelia*** afzelii and B. burgdorferi sensu stricto genotypes, is related to binding of the complement inhibitor factor H to the spirochete. . . key binding regions of the OspE family indicated that several lysine residues are required for factor H binding. Thus, the ***borrelial*** OspE family proteins bind the C inhibitor factor H via multiple sites in a lysine-dependent manner. The C-terminal site V. . . forms a basis for the development of vaccines that block the factor H-OspE interaction and thereby promote the killing of ***Borreliae*** .
CT . . . GE, genetics
*Bacterial Outer Membrane Proteins: ME, metabolism
Bacterial Proteins: GE, genetics
*Bacterial Proteins: ME, metabolism
Blood Proteins: ME, metabolism
*** Borrelia burgdorferi: GE, genetics***
****Borrelia burgdorferi: ME, metabolism***
*** Borrelia burgdorferi: PY, pathogenicity***
Complement Factor H: AI, antagonists & inhibitors
*Complement Factor H: ME, metabolism
Consensus Sequence
Heparin: PD,. . .
RN ***133483-07-5 (VMP21 antigen, Borrelia)*** ; 56-87-1 (Lysine); 80295-65-4 (Complement Factor H); 9005-49-6 (Heparin)
CN 0 (Antigens, Bacterial); 0 (Bacterial Outer Membrane Proteins); 0 (Bacterial Proteins); 0 (Blood Proteins); 0 (Lipoproteins); 0 (OspE protein, ***Borrelia*** burgdorferi); 0 (Peptide Fragments); 0 (Virulence Factors); 0 (complement factor H, human); 0 (factor H-related protein 1)

L4 ANSWER 21 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2005:31487 BIOSIS <<LOGINID::20090609>>
DN PREV200500031306
TI ***Borrelia*** burgdorferi changes its surface antigenic expression in response to host immune responses.
AU Liang, Fang Ting; Yan, Jun; Mbow, M. Lamine; Sviat, Steven L.; Gilmore, Robert D.; Mamula, Mark; Fikrig, Erol [Reprint Author]
CS Sch MedDept Internal MedRheumatol Sect, Yale Univ, S525A,300 Cedar St, New Haven, CT, 06520, USA
erol.fikrig@yale.edu
SO Infection and Immunity, (October 2004) Vol. 72, No. 10, pp. 5759-5767. print.
ISSN: 0019-9567 (ISSN print).
DT Article
LA English
ED Entered STN: 12 Jan 2005
Last Updated on STN: 12 Jan 2005
AB The Lyme disease spirochete, ***Borrelia*** burgdorferi, causes persistent mammalian infection despite the development of vigorous immune responses against the pathogen. To examine spirochetal phenotypes that dominate in the hostile immune environment, the mRNA transcripts of four prototypic surface lipoproteins, decorin-binding protein A (DbpA), outer surface protein C (OspC), BBF01, and VlsE, were analyzed by quantitative reverse transcription-PCR under various immune conditions. We demonstrate that B. burgdorferi changes its surface antigenic expression in response

to immune attack. dbpA expression was unchanged while the spirochetes decreased ospC expression by 446 times and increased BBF01 and vlsE expression up to 20 and 32 times, respectively, under the influence of immune pressure generated in inummocompetent mice during infection. This change in antigenic expression could be induced by passively immunizing infected severe combined immunodeficiency mice with specific ***Borrelia*** antisera or OspC antibody and appears to allow B. burgdorferi to resist immune attack.

TI ***Borrelia*** burgdorferi changes its surface antigenic expression in response to host immune responses.

AB The Lyme disease spirochete, ***Borrelia*** burgdorferi, causes persistent mammalian infection despite the development of vigorous immune responses against the pathogen. To examine spirochetal phenotypes that. . . during infection. This change in antigenic expression could be induced by passively immunizing infected severe combined immunodeficiency mice with specific ***Borrelia*** antisera or OspC antibody and appears to allow B. burgdorferi to resist immune attack.

IT . . .
Lyme disease: bacterial disease, complications, etiology, immunology, pathology
Lyme Disease (MeSH)

IT Chemicals & Biochemicals
BBF01 [VlsE]: expression, prototypic surface lipoprotein; ***Vmp*** -like sequence, expressed [VlsE]; decorin-binding protein A [DbpA]: expression, prototypic surface lipoprotein; mRNA [messenger RNA]; outer surface protein C [OspC]: expression,. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi (species): pathogen, strain-B31 clone 5A11

Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Borrelia*** burgdorferi BBF01 gene (Spirochaetaceae);
Borrelia burgdorferi actin gene (Spirochaetaceae);
Borrelia burgdorferi dbpA gene [***Borrelia*** burgdorferi decorin-binding protein A gene] (Spirochaetaceae); ***Borrelia*** burgdorferi flaB gene (Spirochaetaceae); ***Borrelia*** burgdorferi ospC gene [***Borrelia*** burgdorferi outer surface protein A gene] (Spirochaetaceae); ***Borrelia*** burgdorferi vlsE gene [***Borrelia*** burgdorferi ***Vmp*** -like sequence, expressed gene] (Spirochaetaceae)

L4 ANSWER 22 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 12

AN 2003:153698 BIOSIS <<LOGINID::20090609>>

DN PREV200300153698

TI Characterization of the ***vls*** antigenic variation loci of the Lyme disease spirochaetes ***Borrelia*** garinii Ip90 and ***Borrelia*** afzelii ACAI.

AU Wang, Dachun; Botkin, Douglas J.; Norris, Steven J. [Reprint Author]

CS Department of Pathology and Laboratory Medicine, Medical School at Houston, University of Texas, PO Box 20708, Houston, TX, 77225-0708, USA

Steven.J.Norris@uth.tmc.edu
SO Molecular Microbiology, (March 2003) Vol. 47, No. 5, pp. 1407-1417. print.
ISSN: 0950-382X (ISSN print).
DT Article
LA English
ED Entered STN: 26 Mar 2003
Last Updated on STN: 26 Mar 2003
AB The ***vls*** locus of ***Borrelia*** burgdorferi B31 consists of 15 silent cassettes and one expression site (vlsE), and the presence of the encoding plasmid lp28-1 correlates with high infectivity. Recombination between the expression cassette and silent cassettes occurs in vivo, and this process may enable B. burgdorferi to evade the immune response. To determine the characteristics of the ***vls*** loci in other ***Borrelia*** strains, we have cloned and characterized the ***vls*** silent cassette loci of ***Borrelia*** garinii Ip90 and ***Borrelia*** afzelii ACAI, consisting of 11 ***vls*** silent cassettes and 14 ***vls*** silent cassettes respectively. The silent cassettes share 90-97% nucleotide sequence identity with one another within the Ip90 ***vls*** locus and 84-91% within the ACAI ***vls*** locus. In both organisms, the silent cassettes resemble the B31 ***Vls*** sequences in overall amino acid similarity (50-65%) and in the
presence of six variable regions interspersed between six relatively invariant regions. The vise expression sites of these two strains have not been isolated, but transcripts of vise were detected by reverse transcriptase-polymerase chain reaction for both Ip90 and ACAI. In addition, the occurrence of sequence variation within the vlsE cassette region of these transcripts was verified. This study indicates that the ***vls*** loci present in B. garinii Ip90 and B. afzelii ACAI have characteristics similar to those found in B. burgdorferi B31.
TI Characterization of the ***vls*** antigenic variation loci of the Lyme disease spirochaetes ***Borrelia*** garinii Ip90 and ***Borrelia*** afzelii ACAI.
AB The ***vls*** locus of ***Borrelia*** burgdorferi B31 consists of 15 silent cassettes and one expression site (vlsE), and the presence of the encoding plasmid lp28-1. . . in vivo, and this process may enable B. burgdorferi to evade the immune response. To determine the characteristics of the ***vls*** loci in other ***Borrelia*** strains, we have cloned and characterized the ***vls*** silent cassette loci of ***Borrelia*** garinii Ip90 and ***Borrelia*** afzelii ACAI, consisting of 11 ***vls*** silent cassettes and 14 ***vls*** silent cassettes respectively. The silent cassettes share 90-97% nucleotide sequence identity with one another within the Ip90 ***vls*** locus and 84-91% within the ACAI ***vls*** locus. In both
organisms, the silent cassettes resemble the B31 ***Vls*** sequences in overall amino acid similarity (50-65%) and in the presence of six variable regions interspersed between six relatively invariant. . . . the occurrence of sequence variation within the vlsE cassette region of these transcripts was verified. This study indicates that the ***vls*** loci present in B. garinii Ip90 and B. afzelii ACAI have characteristics similar to those found in B. burgdorferi B31.
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name

Borrelia afzelii (species): parasite, strain-ACAI
Borrelia burgdorferi (species): parasite, B31
Borrelia garinii (species): parasite, strain-Ip90
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***vls*** gene: antigenic variation loci

L4 ANSWER 23 OF 87 CABA COPYRIGHT 2009 CABI on STN DUPLICATE 13
AN 2003:147583 CABA <<LOGINID::20090609>>
DN 20033120690
TI Evaluation of a canine C6 ELISA Lyme disease test for the determination of the infection status of cats naturally exposed to ***Borrelia*** burgdorferi
AU Levy, S. A.; O'Connor, T. E.; Hanscom, J. L.; Shields, P.
CS Durham Veterinary Hospital PC, 178 Parmelee Hill Road, Durham, CT 06422, USA.
SO Veterinary Therapeutics, (2003) Vol. 4, No. 2, pp. 172-177. 27 ref.
Publisher: Veterinary Learning Systems Inc. Trenton
ISSN: 1528-3593
CY United States
DT Journal
LA English
ED Entered STN: 16 Sep 2003
Last Updated on STN: 16 Sep 2003
AB The efficacy of a commercially available in-office kit (SNAP 3Dx, IDEXX Laboratories) for detection of antibodies directed against an invariable region (IR6) of the B. burgdorferi surface protein VlsE (***Vmp*** -like sequence, Ex pressed), a surface antigen of the spirochete recognized during active infection has been evaluated in dogs. The present study was conducted to determine whether this in-office test could be useful for detection of antibodies to B. burgdorferi in cats. Cats owned by clients of a veterinary hospital located in an area hyperendemic for Lyme disease were included in the study. When possible, cats with an outdoor lifestyle, bite wounds, or current tick infestation were recruited for the study to help ensure that animals with a likelihood of exposure to natural infection by B. burgdorferi would be included in the test group. Of the 24 cats tested, 17 samples were positive for antibodies to B. burgdorferi by the C6 ELISA kit. For all 17 of these samples, a duplicate sample tested by immunofluorescent assay (IFA) was in agreement with the ELISA. Five samples were negative by both assays. Two samples that were negative by the C6 ELISA test had low IFA titers (1:100). One of these two discrepant samples was negative and one was positive for antibodies to B. burgdorferi by the Western blot test. It was concluded that the C6 ELISA test performed with good agreement with the IFA and Western blot tests for detection of antibody to B. burgdorferi in the majority of cats tested. The test offers the advantages of producing a result rapidly (approximately 8 minutes), and it requires only two drops of serum, plasma, or whole blood.
TI . . . of a canine C6 ELISA Lyme disease test for the determination of the infection status of cats naturally exposed to ***Borrelia*** burgdorferi.
AB . . . 3Dx, IDEXX Laboratories) for detection of antibodies directed against an invariable region (IR6) of the B. burgdorferi surface protein VlsE (***Vmp*** -like sequence, Ex pressed), a surface antigen of the spirochete recognized during active infection has been evaluated in dogs. The present. . .
BT ***Borrelia*** ; Spirochaetaceae; Spirochaetales; Gracilicutes;

bacteria; prokaryotes; Felis; Felidae; Fissipeda; carnivores; mammals; vertebrates; Chordata; animals; small mammals
ORGN ***Borrelia*** burgdorferi; cats

L4 ANSWER 24 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2002:523404 BIOSIS <<LOGINID::20090609>>
DN PREV200200523404
TI ***VMP*** -like sequences of pathogenic ***borrelia*** .
AU Norris, Steven J. [Inventor, Reprint author]; Zhang, Jing-Ren [Inventor]; Hardham, John M. [Inventor]; Howell, Jerrilyn K. [Inventor]; Barbour, Alan G. [Inventor]; Weinstock, George M. [Inventor]
CS Houston, TX, USA
ASSIGNEE: Board of Regents, The University of Texas System
PI US 6437116 20020820
SO Official Gazette of the United States Patent and Trademark Office Patents, (Aug. 20, 2002) Vol. 1261, No. 3.
http://www.uspto.gov/web/menu/patdata.html. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.
DT Patent
LA English
ED Entered STN: 9 Oct 2002
Last Updated on STN: 9 Oct 2002
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the production of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the deletion of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
TI ***VMP*** -like sequences of pathogenic ***borrelia*** .
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
IT Major Concepts
Infection; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
DNA sequences; ***Vmp*** -like polypeptides
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia : pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 25 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 14
AN 2002:452514 BIOSIS <<LOGINID::20090609>>
DN PREV200200452514
TI Evidence that the variable regions of the central domain of VlsE are antigenic during infection with Lyme disease spirochetes.

AU McDowell, John V.; Sung, Shian-Ying; Hu, Linden T.; Marconi, Richard T. [Reprint author]
CS Department of Microbiology and Immunology, Medical College of Virginia at Virginia Commonwealth University, Richmond, VA, 23298-0678, USA rmarconi@hsc.vcu.edu
SO Infection and Immunity, (August, 2002) Vol. 70, No. 8, pp. 4196-4203. print.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 21 Aug 2002
Last Updated on STN: 21 Aug 2002
AB It has been postulated that the ***vls*** system of the Lyme disease spirochetes contributes to immune evasion through antigenic variation. While it is clear that vlsE undergoes sequence change within its variable regions at a high frequency during the early stages of infection, a definitive role in immune evasion has not been demonstrated. In this report we assessed the murine and human humoral immune response to recombinant (r)-VlsE variants that originally arose during infection in mice. Immunoblot analyses of r-VlsE variants were conducted by using serum samples collected from mice infected with ***Borrelia*** burgdorferi clones that carried different vlsE variants. All of the r-VlsE variants were recognized by infection sera regardless of the identity of the infecting clone or isolate. In addition, all variants were immunoreactive with a panel of human Lyme disease patient serum samples. It is evident from these analyses that the infection-induced VlsE variants share common epitopes that reside within conserved segments of these proteins. However, preabsorption experiments revealed that the variable regions of the central domain of VlsE, which undergo rapid mutation during infection, also influence the antigenic properties of the protein. A subset of the antibodies elicited against vlsE variants that differ in the sequences of their variable regions were found to be variant specific. Hence, in spite of a robust antibody response to conserved segments of VlsE, infection-induced sequence changes within the variable regions alter the antigenicity of VlsE. These results provide the first direct evidence of antigenic variation in the VlsE protein.
AB It has been postulated that the ***vls*** system of the Lyme disease spirochetes contributes to immune evasion through antigenic variation. While it is clear that vlsE undergoes. . . during infection in mice. Immunoblot analyses of r-VlsE variants were conducted by using serum samples collected from mice infected with ***Borrelia*** burgdorferi clones that carried different vlsE variants. All of the r-VlsE variants were recognized by infection sera regardless of the. . .
GEN ***Borrelia*** burgdorferis vlsE gene (Spirochaetaceae)

L4 ANSWER 26 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 15
AN 2002:231270 BIOSIS <<LOGINID::20090609>>
DN PREV200200231270
TI The 44-kb linear plasmid molecule in the relapsing fever agent ***Borrelia*** duttonii strain Ly serve as a preservation of ***vmp*** genes.
AU Tabuchi, Norihiko; Mitani, Harumi; Seino, Satoshi; Fukunaga, Masahito [Reprint author]
CS Laboratory of Molecular Microbiology, Faculty of Pharmacy and Pharmaceutical Sciences, Fukuyama University, Gakuencho 1, Fukuyama,

Hiroshima, 729-0292, Japan
mfukunag@supernig.nig.ac.jp
SO Microbiology and Immunology, (2002) Vol. 46, No. 3, pp. 159-165. print.
CODEN: MIIMDV. ISSN: 0385-5600.
DT Article
LA English
ED Entered STN: 3 Apr 2002
Last Updated on STN: 3 Apr 2002
AB ***Borrelia*** duttonii strain Ly, a causative agent of relapsing fever, contains a linear one megabase chromosome and 12 linear plasmid molecules. Here we report that the sequence of the 44-kb linear plasmid of strain Ly is found to contain variable major protein (***vmp***) genes for antigenic variation of relapsing fever ***borreliae*** . The determined sequence is of 44,010 bp except for both ends of the molecule. Of 39 open reading frames (ORFs) found in the sequence, 21 ORFs (named ***vmpA*** to U) showed moderate similarities with ***vmp*** genes for ***Borrelia*** hermsii. However, most of the ***vmp*** homologues are apparently nonfunctional because of their frameshifts within the sequence and/or absence of promoter and ribosome-binding signals upstream of their genes. RT-PCR experiments using the specific primer for each ***vmp*** gene revealed that ***vmpE*** , one of the ***vmp*** genes, was expressed at the location of the 44-kb plasmid molecule. The result suggests that the plasmid molecule may play a role in the preservation of the serotype switching of ***vmp*** genes in a mammalian host.
TI The 44-kb linear plasmid molecule in the relapsing fever agent ***Borrelia*** duttonii strain Ly serve as a preservation of ***vmp*** genes.
AB ***Borrelia*** duttonii strain Ly, a causative agent of relapsing fever, contains a linear one megabase chromosome and 12 linear plasmid molecules.. . . we report that the sequence of the 44-kb linear plasmid of strain Ly is found to contain variable major protein (***vmp***) genes for antigenic variation of relapsing fever ***borreliae*** . The determined sequence is of 44,010 bp except for both ends of the molecule. Of 39 open reading frames (ORFs) found in the sequence, 21 ORFs (named ***vmpA*** to U) showed moderate similarities with ***vmp*** genes for ***Borrelia*** hermsii. However, most of the ***vmp*** homologues are apparently nonfunctional because of their frameshifts within the sequence and/or absence of promoter and ribosome-binding signals upstream of their genes. RT-PCR experiments using the specific primer for each ***vmp*** gene revealed that ***vmpE*** , one of the ***vmp*** genes, was expressed at the location of the 44-kb plasmid molecule. The result suggests that the plasmid molecule may play a role in the preservation of the serotype switching of ***vmp*** genes in a mammalian host.
IT . . .
RT-PCR [reverse transcriptase-polymerase chain reaction]: analytical method, genetic method, polymerase chain reaction
IT Miscellaneous Descriptors
open reading frames; plasmid sequence; ***vmp*** gene preservation [variable major protein gene preservation]
ORGN . . .
Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia duttonii: pathogen, strain-Ly
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 27 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:791027 CAPLUS <<LOGINID::20090609>>
DN 136:304895
TI Analysis of ***Borrelia*** burgdorferi vlsE gene expression and recombination in the tick vector
AU Indest, Karl J.; Howell, Jerrilyn K.; Jacobs, Mary B.; Scholl-Meeker, Dorothy; Norris, Steven J.; Philipp, Mario T.
CS Department of Parasitology, Tulane Regional Primate Research Center, Tulane University Health Sciences Center, Covington, LA, 70433, USA
SO Infection and Immunity (2001), 69(11), 7083-7090
CODEN: INFIBR; ISSN: 0019-9567
PB American Society for Microbiology
DT Journal
LA English
AB Expression and recombination of the antigenic variation vlsE gene of the Lyme disease spirochete ***Borrelia*** burgdorferi were analyzed in the tick vector. To assess vlsE expression, Ixodes scapularis nymphs infected with the B. burgdorferi strain B31 were fed on mice for 48 or 96 h or to repletion, and then crushed and acetone fixed either immediately thereafter (ticks collected at the two earlier time points) or 4 days after repletion. Unfed nymphs also were examd. At all of the time points investigated, spirochetes were able to bind a rabbit antibody raised against the conserved invariable region 6 of VlsE, as assessed by indirect immunofluorescence, but not pre-immune serum from the same rabbit. This same antibody also bound to B31 spirochetes cultivated in vitro. Intensity of fluorescence appeared highest in cultured spirochetes, followed by spirochetes present in unfed ticks. Only a dim fluorescent signal was obsd. on spirochetes at the 48 and 96 h time points and at day 4 post-repletion. Expression of vlsE in vitro was affected by a rise in pH from 7.0 to 8.0 at 34.degree.C. Hence, vlsE expression appears to be sensitive to environmental cues of the type found in the B. burgdorferi natural history. To assess vlsE recombination, nymphs were capillary fed the B. burgdorferi B31 clonal isolate 5A3. Ticks thus infected were either left to rest for 4 wk (Group I) or fed to repletion on a mouse (Group II). The contents of each tick from both groups were cultured and 10 B. burgdorferi clones from the spirochetal isolate of each tick were obtained. The vlsE cassettes from several of these clones were amplified by PCR and sequenced. Regardless of whether the isolate was derived from Group I or Group II ticks, no changes were obsd. in the vlsE sequence. In contrast, vlsE cassettes amplified from B. burgdorferi clones derived from a mouse that was infected with B31-5A3 capillary-fed nymphs showed considerable recombination. It follows that vlsE recombination does not occur in the tick vector.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Analysis of ***Borrelia*** burgdorferi vlsE gene expression and recombination in the tick vector
AB Expression and recombination of the antigenic variation vlsE gene of the Lyme disease spirochete ***Borrelia*** burgdorferi were analyzed in the tick vector. To assess vlsE expression, Ixodes scapularis nymphs

infected with the B. burgdorferi strain. . .
ST DNA sequence ***Borrelia*** gene vlsE mouse infection tick; ***Borrelia*** gene vlsE lipoprotein tick expression; protein sequence gene vlsE lipoprotein ***Borrelia*** ; genetic recombination ***Borrelia*** gene vlsE mouse infection tick
IT Ixodes scapularis
(anal. of ***Borrelia*** burgdorferi vlsE gene expression and recombination in tick vector)
IT Lipoproteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene vlsE, for ***Vmp*** -like sequence; partial sequence and expression in tick of ***Borrelia*** burgdorferi gene vlsE lipoprotein)
IT Development, nonmammalian postembryonic
(nymph; anal. of ***Borrelia*** burgdorferi vlsE gene expression and recombination in tick vector)
IT ***Borrelia*** burgdorferi
DNA sequences
Protein sequences
(partial sequence of ***Borrelia*** burgdorferi gene vlsE lipoprotein isolated from mouse infected by infestation with Ixodes scapularis nymphal ticks)
IT Lyme disease
Mus
Recombination, genetic
(vlsE cassettes amplified from ***Borrelia*** burgdorferi clones derived from mouse infected with B31-5A3 capillary-fed nymphs showed considerable recombination)
IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(vlsE; partial DNA sequence, expression and recombination in tick vector of ***Borrelia*** burgdorferi gene vlsE)
IT 411243-31-7 411243-32-8 411243-33-9 411243-34-0
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; partial sequence of ***Borrelia*** burgdorferi gene vlsE lipoprotein isolated from mouse infected by infestation with Ixodes scapularis nymphal ticks)
IT 359572-33-1, GenBank AY043397 359572-34-2, GenBank AY043398
359572-35-3, GenBank AY043399 359572-36-4, GenBank AY043400
382261-30-5, GenBank AY043401
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; partial DNA sequence, expression and recombination in tick vector of ***Borrelia*** burgdorferi gene vlsE)

L4 ANSWER 28 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 16
AN 2001:494794 BIOSIS <<LOGINID::20090609>>
DN PREV20100494794
TI Evidence for the contribution of point mutations to vlsE variation and for apparent constraints on the net accumulation of sequence changes in vlsE during infection with Lyme disease spirochetes.
AU Sung, Shian-Ying; McDowell, John V.; Marconi, Richard T. [Reprint author]

CS Department of Microbiology and Immunology, Medical College of Virginia at Virginia Commonwealth University, Richmond, VA, 23298-0678, USA
rmarconi@hsc.vcu.edu
SO Journal of Bacteriology, (October, 2001) Vol. 183, No. 20, pp. 5855-5861. print.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
OS Genbank-AF354775; Genbank-AF354776; Genbank-AF354777; Genbank-AF354778; Genbank-AF354779; Genbank-AF354780; Genbank-AF354781; Genbank-AF354782; Genbank-AF354783; Genbank-AF354784; Genbank-AF354785; Genbank-AF354786; Genbank-AF354787; Genbank-AF354788; Genbank-AF354789; Genbank-AF354790; Genbank-AF354791; Genbank-AF354792; Genbank-AF354793
ED Entered STN: 24 Oct 2001
Last Updated on STN: 25 Feb 2002
AB In the Lyme disease spirochetes, both the ospE and vlsE gene families have been demonstrated to undergo sequence variation during infection. To further investigate the mechanisms associated with the generation of ***vls*** variation, single-nucleotide polymorphism and subsequent DNA sequence analyses were performed on the vlsE gene and its paralog, BBJ51, a related gene with a frameshift mutation. These analyses focused on a series of postinfection clonal populations obtained from mice infected with ***Borrelia*** burgdorferi B31MIpc or its clonal derivative, B31MIc53. vlsE, but not BBJ51, was found to undergo sequence changes during infection. Consistent with that reported previously (J.-R. Zhang et al., Cell 89:275-285, 1997) many of the sequence changes appear to have arisen through gene conversion events and to be localized to the variable regions of vlsE. However, analysis of the vlsE nucleotide sequences revealed that some sequence changes were the result of point mutations, as these changes did not have potential contributing sources in the ***vls*** cassettes. To determine if sequence changes accumulate in vlsE over long-term infection, the vlsE genes of clonal populations recovered after 7 months of infection in mice were analyzed. While new sequence changes developed, a significant number of these changes resulted in the restoration of the vlsE sequence of the original infecting clone. In addition, we noted that some positions within the variable regions (VR) are stable even though the cassettes possess residues that could contribute to sequence variation through gene conversion. These analyses suggest that the total number of amino acid sequence changes that can be maintained by VlsE levels off during infection. In summary, in this report we demonstrate that the development of point mutations serves as a second mechanism by which vlsE sequence variation can be generated and that the capacity for vlsE variation, while still significant, is less than previously postulated.
AB. . . families have been demonstrated to undergo sequence variation during infection. To further investigate the mechanisms associated with the generation of ***vls*** variation, single-nucleotide polymorphism and subsequent DNA sequence analyses were performed on the vlsE gene and its paralog, BBJ51, a related. . . gene with a frameshift mutation. These analyses focused on a series of postinfection clonal populations obtained from mice infected with ***Borrelia*** burgdorferi B31MIpc or its clonal derivative, B31MIc53. vlsE, but not BBJ51, was found to undergo sequence changes during infection. Consistent. . . some sequence changes were the result of point mutations, as these changes did not have potential contributing sources in the ***vls*** cassettes. To determine if sequence changes accumulate in vlsE over long-term infection, the vlsE genes of clonal populations recovered after. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi: pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***Borrelia*** burgdorferi vlsE gene (Spirochaetaceae): frameshift mutation, point mutation, sequence changes

L4 ANSWER 29 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:695183 CAPLUS <<LOGINID::20090609>>
DN 135:370510
TI ***Borrelia*** burgdorferi-induced inflammation facilitates spirochete adaptation and variable major protein-like sequence locus recombination
AU Anguita, Juan; Thomas, Venetta; Samanta, Swapna; Persinski, Rafal; Hernanz, Carmen; Barthold, Stephen W.; Fikrig, Erol
CS Section of Rheumatology, Department of Internal Medicine, Yale University School of Medicine, New Haven, CT, 06520, USA
SO Journal of Immunology (2001), 167(6), 3383-3390
CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB Spirochete adaptation in vivo is assocd. with preferential B. burgdorferi gene expression. Here, the authors show that the administration of B. burgdorferi-immune sera to IFN-.gamma.R-deficient mice that have been infected with B. burgdorferi N40 for 4 days causes spirochete clearance. In contrast, immune sera-mediated clearance of B. burgdorferi N40 is not apparent in immunocompetent mice, suggesting a role for IFN-.gamma.-mediated responses in B. burgdorferi N40 host adaptation. B. burgdorferi-immune sera also induce clearance of B. burgdorferi N40 that have been passaged in vitro 75 times (B. burgdorferi N40-75), a deriv. of B. burgdorferi N40 that does not rapidly adapt in vivo in immunocompetent mice. B. burgdorferi N40-75 produces lower levels of IFN-.gamma. and IL-12 in mice than does B. burgdorferi N40, and the administration of these cytokines to B. burgdorferi N40-75-infected mice results in an increased spirochetal burden, further indicating that IFN-.gamma.-mediated events promote B. burgdorferi survival. Differential immunoscreening and RT-PCR demonstrate that IFN-.gamma.-mediated signals facilitate spirochete recombination at the variable major protein like sequence locus, a site for early antigenic variation in vivo, and that recombination rates by B. burgdorferi N40 are lower in IFN-.gamma.R-deficient mice than in control animals. Thus, the murine immune response can promote the in vivo adaptation of B. burgdorferi.
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI ***Borrelia*** burgdorferi-induced inflammation facilitates spirochete adaptation and variable major protein-like sequence locus recombination
ST ***Borrelia*** adaptation Lyme disease ***vls*** gene recombination cytokine
IT Adaptation, microbial
Borrelia burgdorferi
Inflammation

Recombination, genetic
(***Borrelia*** burgdorferi-induced inflammation facilitates spirochete adaptation and variable major protein-like sequence locus recombination)
IT Signal transduction, biological
(interferon .gamma. signals facilitate ***Borrelia*** burgdorferi recombination at variable major protein like sequence locus)
IT Interleukin 12
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(interferon .gamma./interleukin-12 signals facilitate ***Borrelia*** burgdorferi recombination at variable major protein like sequence locus)
IT Gene, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(***vls*** (variable major protein-like sequence); interferon .gamma. signals facilitate ***Borrelia*** burgdorferi recombination at variable major protein like sequence locus)
IT Interferons
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(.gamma.; interferon .gamma. signals facilitate ***Borrelia*** burgdorferi recombination at variable major protein like sequence locus)

L4 ANSWER 30 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2002:222937 BIOSIS <<LOGINID::20090609>>
DN PREV200200222937
TI Comparative analysis of the kinetics of mutation in the ***vls*** and ospE antigenic variation systems of Lyme disease spirochetes during infection in mice.
AU Sung, S. [Reprint author]; McDowell, J. V. [Reprint author]; Marconi, R. T. [Reprint author]
CS Medical College of VA of VCU, Richmond, VA, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2001) Vol. 101, pp. 325-326. print.
Meeting Info.: 101st General Meeting of the American Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society of Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 3 Apr 2002
Last Updated on STN: 3 Apr 2002
AB The Lyme disease spirochetes possess two potential antigenic variation systems: the ospE gene family and the ***vmp*** -like sequence system (***vls***). To compare the kinetics of mutation in these systems, the vlsE gene was analyzed in a series of post-infection clonal populations in which the kinetics of mutation in the ospE genes had been previously characterized. Prior to initiating these analyses it was necessary to determine if vlsE is carried by B. burgdorferi B31MI and its post-infection clonal populations. These analyses were required because

although the majority of the genome sequence of B31MI has been determined, the segment thought to carry vlsE was neither sequenced or mapped. PCR analyses confirmed the presence of a vlsE and demonstrated that this allele was maintained after 3 months of infection in mice. PCR and hybridization analyses demonstrated that large scale rearrangements in vlsE did not occur over the course of infection. Hybridization analyses of DNA fractionated by two dimensional pulsed field gel electrophoresis demonstrated vlsE to be carried on the linear plasmid, lp28-1. To assess vlsE genetic stability, vlsE was amplified from post-infection clones recovered from ear punch biopsies from mice infected with B31MI and the amplicons were screened for polymorphisms. Genetic changes were detected and a comparision of the mutation rates in vlsE and ospE revealed that the vlsE gene undergoes mutation at a higher frequency than ospE. A silent B. burgdorferi B31MI ***vls*** allele, vlsE1, which harbors an frameshift mutation, was found to be genetically stable. To determine if mutations continue to accumulate over long term infection, a clone recovered from the ear punch biopsy was used to infect a mouse and the infection was allowed to persist for 7 months. Analysis of vlsE from the clonal populations recovered at 7 months revealed that while some new mutations developed many of the genetic changes were in the form of reversions. These analyses suggest that there is a limit to the accumulation of mutations in the vlsE gene and that the potential number of variants that can arise may not be as great as previously postulated.

TI Comparative analysis of the kinetics of mutation in the ***vls*** and ospE antigenic variation systems of Lyme disease spirochetes during infection in mice.

AB The Lyme disease spirochetes possess two potential antigenic variation systems: the ospE gene family and the ***vmp*** -like sequence system (***vls***). To compare the kinetics of mutation in these systems, the vlsE gene was analyzed in a series of post-infection clonal. . . and ospE revealed that the vlsE gene undergoes mutation at a higher frequency than ospE. A silent B. burgdorferi B31MI ***vls*** allele, vlsE1, which harbors an frameshift mutation, was found to be genetically stable. To determine if mutations continue to accumulate. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi: pathogen

Taxa Notes
Bacteria, Eubacteria, Microorganisms

GEN ***Borrelia*** burgdorferi ospE gene (Spirochaetaceae): analysis, mutation; ***Borrelia*** burgdorferi vlsE gene (Spirochaetaceae): analysis, mutation

L4 ANSWER 31 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 17

AN 2001:372097 BIOSIS <<LOGINID::20090609>>

DN PREV200100372097

TI Increased expression of ***Borrelia*** burgdorferi vlsE in response to human endothelial cell membranes.

AU Hudson, Charlene R.; Frye, Jonathan G.; Quinn, Frederick D.; Gherardini, Frank C. [Reprint author]

CS Department of Microbiology, University of Georgia, 546 Biological Sciences

Building, Athens, GA, 30602, USA
FRANKG@arches.uga.edu
SO Molecular Microbiology, (July, 2001) Vol. 41, No. 1, pp. 229-239. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
OS Genbank-AF314755
ED Entered STN: 8 Aug 2001
Last Updated on STN: 19 Feb 2002
AB RNA isolated from virulent ***Borrelia*** burgdorferi cells incubated with human endothelial or neurological tissue cells was subjected to subtractive hybridization using RNA from the same strain incubated in tissue culture medium alone. This RNA subtractive technique generated specific probes that hybridized to two restriction fragments (8.2 kb and 10 kb respectively) generated by EcoRI digestion of total plasmid DNA. The 10 kb EcoRI fragment localized to Ip28-1 and was subsequently identified as the variable membrane protein-like sequence (***vls***) region, which includes an expression locus (vlsE) and 15 silent cassettes. vlsE encodes a 36 kDa outer surface protein that undergoes antigenic variation during animal infections. Primer extension analysis identified the 5' end of a transcript and a putative promoter for vlsE. Quantitative reverse transcription-polymerase chain reaction (RT-PCR) suggested that the expression of vlsE increased when virulent B. burgdorferi cells were incubated with human tissue cells or purified cell membranes isolated from those same cell lines. A 138 bp region upstream of the vlsE region that was not reported in the genome sequence was sequenced using specific 32P end-labelled primers in a DNA cycle sequencing system at high annealing temperatures. Analysis revealed that it contained a 51 bp inverted repeat, which could form an extremely stable cruciform structure. Southern blots probed with the vlsE promoter/operator region indicated that part or all of this sequence could be found on other B. burgdorferi plasmids.
TI Increased expression of ***Borrelia*** burgdorferi vlsE in response to human endothelial cell membranes.
AB RNA isolated from virulent ***Borrelia*** burgdorferi cells incubated with human endothelial or neurological tissue cells was subjected to subtractive hybridization using RNA from the same. . . plasmid DNA. The 10 kb EcoRI fragment localized to Ip28-1 and was subsequently identified as the variable membrane protein-like sequence (***vls***) region, which includes an expression locus (vlsE) and 15 silent cassettes. vlsE encodes a 36 kDa outer surface protein that. . .
GEN ***Borrelia*** burgdorferi vlsE gene (Spirochaetaceae): expression

L4 ANSWER 32 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 18
AN 2001:355831 BIOSIS <<LOGINID::20090609>>
DN PREV200100355831
TI Analysis of a ***VMP*** -like sequence (***vls***) locus in ***Borrelia*** garinii and ***Vls*** homologues among four ***Borrelia*** burgdorferi sensu lato species.
AU Wang, Guiqing [Reprint author]; van Dam, Alje P.; Dankert, Jacob
CS Department of Biochemistry and Molecular Biology, New York Medical College, Valhalla, NY, 10595, USA
guiqing_wang@nymc.edu
SO FEMS Microbiology Letters, (15 May, 2001) Vol. 199, No. 1, pp. 39-45. print.
CODEN: FMLED7. ISSN: 0378-1097.

DT Article
LA English
OS Genbank-AF274070; Genbank-AF274071; Genbank-AF274072; Genbank-AF274073; Genbank-AF274074; Genbank-AF274075; Genbank-AF274076
ED Entered STN: 2 Aug 2001
Last Updated on STN: 23 Feb 2002
AB The ***VMP*** -like sequence (***vls***) locus that consists of one expressed vlsE gene and 15 silent ***vls*** cassettes has been described in ***Borrelia*** burgdorferi sensu stricto B31. In the present study, the ***vls*** locus from a ***Borrelia*** garinii isolate A87SA was analyzed. DNA fragments that contained three complete and five partial ***vls*** cassettes were cloned and sequenced. Pulsed-field gel electrophoresis (PFGE) analysis and Southern hybridization of the PFGE blot indicated that the ***vls*** locus of B. garinii A87SA, consisting of at least eight ***vls*** cassettes, was located on a 21-kb linear plasmid. The size of the three complete ***vls*** cassettes varied from 573 to 612 bp. They had 93.8-94.3% identity at the nucleotide level and 84.9-87.3% amino acid identity. The amino acid sequences of the three ***vls*** cassettes of B. garinii A87SA exhibited 45.9-50.8% identity to the VlsE sequence of B. burgdorferi B31, and 30.0-33.8% identity to the ***VMP17*** sequence of B. hermsii HS1. Homologues of the ***vls*** locus of B. garinii were detected by dot blot hybridization among 24 of the 30 (80.0%) isolates representing four B. burgdorferi sensu lato species distributed widely in Europe. Our findings indicate that B. garinii might possess a similar ***vls*** structure to that described in B. burgdorferi sensu stricto. The highly conserved nature of the ***vls*** locus among various B. burgdorferi sensu lato species suggests that it may be important in the physiology and pathogenesis of Lyme disease spirochetes.
TI Analysis of a ***VMP*** -like sequence (***vls***) locus in ***Borrelia*** garinii and ***Vls*** homologues among four ***Borrelia*** burgdorferi sensu lato species.
AB The ***VMP*** -like sequence (***vls***) locus that consists of one expressed vlsE gene and 15 silent ***vls*** cassettes has been described in ***Borrelia*** burgdorferi sensu stricto B31. In the present study, the ***vls*** locus from a ***Borrelia*** garinii isolate A87SA was analyzed. DNA fragments that contained three complete and five partial ***vls*** cassettes were cloned and sequenced. Pulsed-field gel electrophoresis (PFGE) analysis and Southern hybridization of the PFGE blot indicated that the ***vls*** locus of B. garinii A87SA, consisting of at least eight ***vls*** cassettes, was located on a 21-kb linear plasmid. The size of the three complete ***vls*** cassettes varied from 573 to 612 bp. They had 93.8-94.3% identity at the nucleotide level and 84.9-87.3% amino acid identity. The amino acid sequences of the three ***vls*** cassettes of B. garinii A87SA exhibited 45.9-50.8% identity to the VlsE sequence of B. burgdorferi B31, and 30.0-33.8% identity to the ***VMP17*** sequence of B. hermsii HS1. Homologues of the ***vls*** locus of B. garinii were detected by dot blot hybridization among 24 of the 30 (80.0%) isolates representing four B. burgdorferi sensu lato species distributed widely in Europe. Our findings indicate that B. garinii might possess a similar ***vls*** structure to that described in B. burgdorferi sensu stricto. The highly conserved nature of the ***vls*** locus among various B. burgdorferi sensu lato species suggests that it may be important in the physiology and pathogenesis of. . .
ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi: pathogen
Borrelia garinii: pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms
GEN ***Borrelia*** garinii ***vls*** gene (Spirochaetaceae);
Borrelia garinii vlsE gene (Spirochaetaceae)

L4 ANSWER 33 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:911291 CAPLUS <<LOGINID::20090609>>
DN 134:70362
TI Combined decorin binding protein and outer surface protein compositions and methods of use
IN Hanson, Mark S.; Patel, Nita K.; Cassatt, David R.
PA Medimmune, Inc., USA
SO PCT Int. Appl., 111 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000078800	A2	20001228	WO 2000-US16763	20000616
WO 2000078800	A3	20010719		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-140258P P 19990618
AB Disclosed are surprisingly effective compns., therapeutic kits and vaccines comprising one or more ***Borrelia*** decorin binding protein components and one or more ***Borrelia*** outer surface protein components. Methods and medical uses are also disclosed in which the compns., kits and vaccines are administered to prevent and/or treat ***Borrelial*** infections, notably the ***Borrelial*** infections that cause Lyme disease.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB Disclosed are surprisingly effective compns., therapeutic kits and vaccines comprising one or more ***Borrelia*** decorin binding protein components and one or more ***Borrelia*** outer surface protein components. Methods and medical uses are also disclosed in which the compns., kits and vaccines are administered to prevent and/or treat ***Borrelial*** infections, notably the ***Borrelial*** infections that cause Lyme disease.
ST ***Borrelia*** decorin binding protein DbpA vaccine; outer surface protein OspA ***Borrelia*** vaccine
IT Decorins
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(-binding protein; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(DbpA; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(DbpB; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(EppA; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT ***Borrelia*** garinii
(G25; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Lipoproteins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(Osp or outer surface proteins; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Lipoproteins
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(OspA or outer surface protein A; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Lipoproteins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(OspB or outer surface protein B; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Lipoproteins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(OspC or outer surface protein C; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Lipoproteins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(OspD or outer surface protein D; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Lipoproteins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(OspE or outer surface protein E; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Lipoproteins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(OspF or outer surface protein F; combination of decorin binding

protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(S1; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(T5; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(***Vmp7*** ; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Immunostimulants
(adjuvants; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Animal
Borrelia
Borrelia afzelii
Borrelia burgdorferi
Drug delivery systems
Lyme disease
Molecular cloning
Vaccines
(combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Antibodies
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Flagellins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Medical goods
(containers; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(decorin-binding; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Immunoglobulins
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(fragments; combination of decorin binding protein and outer surface

protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Drug delivery systems
(injections, intradermal; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Drug delivery systems
(injections, s.c.; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Containers
(medical; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Drug delivery systems
(nasal, intra-; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(p110; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(p13; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(p17; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(p28; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(p35; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(p37; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(p39 .alpha.; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

IT Proteins, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(p39 .beta.; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia***

infection or Lyme disease)

IT 7429-90-5, Aluminum, biological studies 21645-51-2, Aluminum hydroxide, biological studies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(adjuvant; combination of decorin binding protein and outer surface protein as vaccine for preventing or treating ***Borrelia*** infection or Lyme disease)

L4 ANSWER 34 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 19
AN 2001:63090 BIOSIS <<LOGINID::20090609>>
DN PREV200100063090
TI Correlation between plasmid content and infectivity in ***Borrelia*** burgdorferi.
AU Purser, Joye E.; Norris, Steven J. [Reprint author]
CS Department of Pathology and Laboratory Medicine, Medical School, and Graduate School of Biomedical, University of Texas-Houston Health Science Center, Houston, TX, 77225, USA
Steven.J.Norris@uth.tmc.edu
SO Proceedings of the National Academy of Sciences of the United States of America, (December 5, 2000) Vol. 97, No. 25, pp. 13865-13870. print.
CODEN: PNASA6. ISSN: 0027-8424.
DT Article
LA English
ED Entered STN: 31 Jan 2001
Last Updated on STN: 12 Feb 2002
AB Infectivity-associated plasmids were identified in ***Borrelia*** burgdorferi B31 by using PCR to detect each of the plasmids in a panel of 19 clonal isolates. The clones exhibited high-, low-, and intermediate-infectivity phenotypes based on their frequency of isolation from needle-inoculated C3H/HeN mice. Presence or absence of 21 of the 22 plasmids was determined in each of the clones by using PCR primers specific for regions unique to each plasmid, as identified in the recently available genome sequence. Southern blot hybridization results were used to confirm the PCR results in some cases. Plasmid lp25 exhibited a direct correlation with infectivity in that it was consistently present in all clones of high or intermediate infectivity and was absent in all low-infectivity clones. lp28-1, containing the ***vmp*** -like sequence locus, also correlated with infectivity; all clones that lacked lp28-1 but contained lp25 had an intermediate infectivity phenotype, in which infection was primarily restricted to the joints. Plasmids cp9, cp32-3, lp21, lp28-2, lp28-4, and lp56 apparently are not required for infection in this model, because clones lacking these plasmids exhibited a high-infectivity phenotype. Plasmids cp26, cp32-1, cp32-2 and/or cp32-7, cp32-4, cp32-6, cp32-8, cp32-9, lp17, lp28-3, lp36, lp38, and lp54 were consistently present in all clones examined. On the basis of these results, lp25 and lp28-1 appear to encode virulence factors important in the pathogenesis of B. burgdorferi B31.
TI Correlation between plasmid content and infectivity in ***Borrelia*** burgdorferi.
AB Infectivity-associated plasmids were identified in ***Borrelia*** burgdorferi B31 by using PCR to detect each of the plasmids in a panel of 19 clonal isolates. The clones. . . consistently present in all clones of high or intermediate infectivity and was absent in all low-infectivity clones. lp28-1, containing the ***vmp*** -like sequence locus, also correlated with infectivity; all clones that lacked lp28-1 but contained lp25 had an intermediate infectivity phenotype, in. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi: pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 35 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 20
AN 2000:452609 BIOSIS <<LOGINID::20090609>>
DN PREV200000452609
TI Direct evidence for involvement of NF-kappaB in transcriptional activation of tumor necrosis factor by a spirochetal lipoprotein.
AU Udalova, Irina A. [Reprint author]; Vidal, Vincent; Scragg, Ian G.; Kwiatkowski, Dominic
CS Molecular Infectious Disease Group, Institute of Molecular Medicine, John Radcliffe Hospital, Oxford, OX3 9DS, UK
SO Infection and Immunity, (September, 2000) Vol. 68, No. 9, pp. 5447-5449. print.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 25 Oct 2000
Last Updated on STN: 10 Jan 2002
AB Variable major lipoprotein (***Vmp***) is a major tumor necrosis factor (TNF)-inducing component of ***Borrelia*** recurrentis, the agent of louse-borne relapsing fever. B. recurrentis ***Vmp*** rapidly stimulates nuclear translocation of NF-kappaB and proinflammatory cytokine gene expression in the human monocyte-like cell line MonoMac 6. By overexpressing disabled mutant IkappaBalpha in MonoMac 6 cells cotransfected with a reporter gene, we provide evidence that NF-kappaB is essential for the transcriptional activation of TNF in this system.
AB Variable major lipoprotein (***Vmp***) is a major tumor necrosis factor (TNF)-inducing component of ***Borrelia*** recurrentis, the agent of louse-borne relapsing fever. B. recurrentis ***Vmp*** rapidly stimulates nuclear translocation of NF-kappaB and proinflammatory cytokine gene expression in the human monocyte-like cell line MonoMac 6. By. . .
ORGN . . .
Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia recurrentis: pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 36 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 21
AN 2000:169153 BIOSIS <<LOGINID::20090609>>

DN PREV200000169153
TI Conservation and heterogeneity of vlsE among human and tick isolates of ***Borrelia*** burgdorferi.
AU Iyer, Radha; Hardham, John M.; Wormser, Gary P.; Schwartz, Ira; Norris, Steven J. [Reprint author]
CS Department of Pathology and Laboratory Medicine, University of Texas Medical School at Houston, Houston, TX, 77225, USA
SO Infection and Immunity, (March, 2000) Vol. 68, No. 3, pp. 1714-1718. print.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 3 May 2000
Last Updated on STN: 4 Jan 2002
AB The ***vls*** (variable major protein (***VMP***)-like sequence) locus of ***Borrelia*** burgdorferi encodes an antigenic variation system that closely resembles the ***VMP*** system of relapsing fever ***borreliae*** . To determine whether ***vls*** sequences are present consistently in low-passage, infectious isolates of B. burgdorferi, 22 blood and erythema migrans biopsy isolates from Lyme disease patients in Westchester County, New York, were examined by Southern blot and PCR analysis. Each of the strains contained a single plasmid varying in size from 21 to 38 kb that hybridized strongly with a vlsE probe based on the B. burgdorferi B31 sequence. In contrast, PCR products were obtained with only 10 of the 22 strains when primers corresponding to the 5' and 3' regions of the B31 vlsE sequence outside the variable cassette region were used. Only 2 of 16 B. burgdorferi-infected tick specimens yielded detectable PCR product. Eight of 10 strains that yielded a PCR product under these conditions were type 1 (a genotype with a high rate of dissemination), according to PCR-restriction fragment length polymorphism analysis of intergenic rDNA sequences, whereas the isolates that did not yield vlsE PCR products were either type 2 or type 3. Comparison of the sequences of cloned PCR products from the patient isolates indicated a high degree of identity to the B31 sequence, with most of the differences restricted to the hypervariable regions known to undergo sequence variation. Taken together, these results both reinforce previous evidence that ***vls*** sequences are present consistently in low-passage Lyme disease spirochetes and indicate that both highly conserved and heterogeneous subgroups exist with regard to vlsE sequences.
TI Conservation and heterogeneity of vlsE among human and tick isolates of ***Borrelia*** burgdorferi.
AB The ***vls*** (variable major protein (***VMP***)-like sequence) locus of ***Borrelia*** burgdorferi encodes an antigenic variation system that closely resembles the ***VMP*** system of relapsing fever ***borreliae*** . To determine whether ***vls*** sequences are present consistently in low-passage, infectious isolates of B. burgdorferi, 22 blood and erythema migrans biopsy isolates from Lyme. . . differences restricted to the hypervariable regions known to undergo sequence variation. Taken together, these results both reinforce previous evidence that ***vls*** sequences are present consistently in low-passage Lyme disease spirochetes and indicate that both highly conserved and heterogeneous subgroups exist with. . .
IT Major Concepts
Infection
IT Diseases
Lyme disease: bacterial disease

Lyme Disease (MeSH)
IT Chemicals & Biochemicals
Borrelia burgdorferi ***vls*** gene; ***Borrelia*** burgdorferi vlsE gene
ORGN . . .
Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi: pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 37 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 22
AN 2000:369051 BIOSIS <<LOGINID::20090609>>
DN PREV200000369051
TI Structural characterization of the inflammatory moiety of a variable major lipoprotein of ***Borrelia*** recurrentis.
AU Scragg, Ian G.; Kwiatkowski, Dominic [Reprint author]; Vidal, Vincent; Reason, Andrew; Paxton, Thanai; Panico, Maria; Dell, Ann; Morris, Howard
CS Dept. of Paediatrics, University of Oxford, John Radcliffe Hospital, Oxford, OX3 9DU, UK
SO Journal of Biological Chemistry, (January 14, 2000) Vol. 275, No. 2, pp. 937-941. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
OS Genbank-AJ237608; EMBL-AJ237608; DDBJ-AJ237608
ED Entered STN: 30 Aug 2000
Last Updated on STN: 8 Jan 2002
AB Louse-borne relapsing fever, caused by ***Borrelia*** recurrentis, provides one of the best documented examples of the causative role of tumor necrosis factor (TNF) in the pathology of severe infection in humans. We have identified the principal TNF-inducing factor of B. recurrentis as a variable major lipoprotein (***Vmp***). Here we report the complete gene sequence of ***Vmp*** , including its lipoprotein leader sequence. Using metabolically labeled forms of the native ***Vmp*** we confirm that the TNF inducing properties are associated with the lipid portion of the molecule. Quadrupole orthogonal time of flight mass spectrometry unequivocally locates the lipidic moiety at the NH2-terminal cysteine of the native polypeptide, and indicates the existence of three forms which are consistent with the structures C16:0, C16:0, C16:0 glyceryl cysteine; C18:1, C16:0, C16:0 glyceryl cysteine; and C18:0, C16:0, C16:0 glyceryl cysteine. These data provide the first direct evidence that the TNF inducing lipid modification of native ***Borrelia*** lipoproteins is a structural homologue of the murein lipoprotein of Escherichia coli.
TI Structural characterization of the inflammatory moiety of a variable major lipoprotein of ***Borrelia*** recurrentis.
AB Louse-borne relapsing fever, caused by ***Borrelia*** recurrentis, provides one of the best documented examples of the causative role of tumor necrosis factor (TNF) in the pathology. . . of severe infection in humans. We have identified the principal TNF-inducing factor of B.

recurrentis as a variable major lipoprotein (***Vmp***). Here we report the complete gene sequence of ***Vmp*** , including its lipoprotein leader sequence. Using metabolically labeled forms of the native ***Vmp*** we confirm that the TNF inducing properties are associated with the lipid portion of the molecule. Quadrupole orthogonal time of. . . C18:0, C16:0, C16:0 glyceryl cysteine. These data provide the first direct evidence that the TNF inducing lipid modification of native ***Borrelia*** lipoproteins is a structural homologue of the murein lipoprotein of Escherichia coli.

IT . . .
and Techniques
IT Diseases
louse borne relapsing fever: bacterial disease
IT Chemicals & Biochemicals
tumor necrosis factor; variable major lipoprotein [***Vmp***]: biochemical structure, structural inflammatory moiety characterization
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia recurrentis
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 38 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2000:388142 BIOSIS <<LOGINID::20090609>>
DN PREV200000388142
TI Characteristics of the ***vls*** locus of ***Borrelia*** garinii Ip90.
AU Wang, D. [Reprint author]; Norris, S. J. [Reprint author]
CS Univ. of Texas Med. School, Houston, TX, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2000) Vol. 100, pp. 275. print.
Meeting Info.: 100th General Meeting of the American Society for Microbiology. Los Angeles, California, USA. May 21-25, 2000. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 13 Sep 2000
Last Updated on STN: 8 Jan 2002
TI Characteristics of the ***vls*** locus of ***Borrelia*** garinii Ip90.
IT Miscellaneous Descriptors
gene expression: analysis; genetic loci: analysis, characterization; ***vls*** locus: analysis, characterization; Meeting Abstract
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia garinii: pathogen, strain-Ip90
Borrelia spp.: pathogen
Taxa Notes

Bacteria, Eubacteria, Microorganisms

L4 ANSWER 39 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 23
AN 1999:809495 CAPLUS <<LOGINID::20090609>>
DN 132:277841
TI Human antibody responses to VlsE antigenic variation protein of ***Borrelia*** burgdorferi
AU Lawrenz, M. B.; Hardham, J. M.; Owens, R. T.; Nowakowski, J.; Steere, A. C.; Wormser, G. P.; Norris, S. J.
CS Departments of Pathology and Laboratory Medicine and Microbiology and Molecular Genetics, University of Texas Medical School at Houston, Houston, TX, 77030, USA
SO Journal of Clinical Microbiology (1999), 37(12), 3997-4004
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB VlsE is a 35-kDa surface-exposed lipoprotein of B. burgdorferi that was shown previously to undergo antigenic variation through segmental recombination of silent ***vls*** cassettes with vlsE during exptl. mouse infections. Previous data had indicated that sera from North American Lyme disease patients and exptl. infected animals contained antibodies reactive with VlsE. Here, sera from patients with Lyme disease, syphilis, and autoimmune conditions as well as from healthy controls were examd. for reactivity with VlsE by Western blotting and ELISA. Strong Western blot reactivity to a recombinant VlsE cassette region protein was obtained consistently with Lyme disease sera. Although sera from Lyme disease patients also reacted with a band corresponding to VlsE in B. burgdorferi B31-5A3, interpretation was complicated by low levels of VlsE expression in in vitro-cultured B. burgdorferi and by the presence of comigrating bands. An ELISA using recombinant VlsE was compared with an ELISA using sonically disrupted B. burgdorferi as the antigen. For a total of 93 Lyme disease patient sera examd., the VlsE ELISA yielded sensitivities of 63% for culture-confirmed erythema migrans cases and 92% for later stages, as compared to 61 and 98%, resp., for the "whole-cell" ELISA. The specificities of the two assays with healthy blood donor sera were comparable, but the VlsE ELISA was 90% specific with sera from syphilis patients, compared to 20% specificity for the whole-cell ELISA with this group. Neither assay showed reactivity with a panel of sera from 20 non-Lyme disease arthritis patients or 20 systemic lupus erythematosus patients. Thus, VlsE may be useful in the immunodiagnosis of Lyme disease and may offer greater specificity than ELISAs using whole B. burgdorferi as the antigen.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Human antibody responses to VlsE antigenic variation protein of ***Borrelia*** burgdorferi
AB . . . a 35-kDa surface-exposed lipoprotein of B. burgdorferi that was shown previously to undergo antigenic variation through segmental recombination of silent ***vls*** cassettes with vlsE during exptl. mouse infections. Previous data had indicated that sera from North American Lyme disease patients and. . .
ST antibody VlsE protein ***Borrelia*** Lyme disease serodiagnosis
IT Gene, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(VlsE; Western blot and ELISA for detection of human antibody responses to VlsE antigenic variation protein of ***Borrelia*** burgdorferi)

IT Antigenic variation
Blood analysis
Borrelia burgdorferi
Lymph disease
(Western blot and ELISA for detection of human antibody responses to VlsE antigenic variation protein of ***Borrelia*** burgdorferi)
IT Antibodies
RL: ANT (Analyte); ANST (Analytical study)
(Western blot and ELISA for detection of human antibody responses to VlsE antigenic variation protein of ***Borrelia*** burgdorferi)
IT Proteins, specific or class
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gene VlsE; Western blot and ELISA for detection of human antibody responses to VlsE antigenic variation protein of ***Borrelia*** burgdorferi)
IT Diagnosis
(serodiagnosis; Western blot and ELISA for detection of human antibody responses to VlsE antigenic variation protein of ***Borrelia*** burgdorferi)

L4 ANSWER 40 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 24
AN 1999:265523 BIOSIS <<LOGINID::20090609>>
DN PREV199900265523
TI Specific antibodies reactive with the 22-kilodalton major outer surface protein of ***Borrelia*** anserina Ni-NL protect chicks from infection.
AU Sambri, Vittorio; Marangoni, Antonella; Olmo, Andrea; Storni, Elisa; Montagnani, Marco; Fabbi, Massimo; Cevenini, Roberto [Reprint author]
CS Section of Microbiology, DMCSS, University of Bologna, St. Orsola Hospital, via Massarenti 9, 40138, Bologna, Italy
SO Infection and Immunity, (May, 1999) Vol. 67, No. 5, pp. 2633-2637. print.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 15 Jul 1999
Last Updated on STN: 15 Jul 1999
AB An outer surface lipoprotein or 22 kDa was identified in the avian pathogen ***Borrelia*** anserina Ni-NL by using antibody preparations reactive with bacterial surface-exposed proteins. Amino acid sequence analysis of the 22-kDa protein demonstrated 90% identity with ***VmpA*** of B. turicatae, suggesting that the protein belongs to the family of 20-kDa outer surface proteins of the genus ***Borrelia*** . All of the 60 chicks intramuscularly treated with antibodies specifically reacting with the 22-kDa protein and infected with strain Ni-NL were completely protected from infection, since no spirochetemia was detected, and from death. Control chicks were treated with immune sera raised against apathogenic strain B. anserina Es, which expresses a prominent 20-kDa polypeptide that is also a member of the ***Vmp*** family but does not cross-react immunologically with the 22-kDa protein of the Ni-NL strain. These animals, infected with B. anserina Ni-NL, showed a high degree of spirochetemia 10 days after infection, and all died between 14 and 21 days after infection. The results showed that the 22-kDa surface protein of B. anserina Ni-NL is a determinant of the pathogenic potential of the strain and also confirmed that only strain-specific antibodies are protective against B. anserina infection.
TI Specific antibodies reactive with the 22-kilodalton major outer surface

protein of ***Borrelia*** anserina Ni-NL protect chicks from infection.

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IT Major Concepts
Infection

IT Diseases
borrelia infection: bacterial disease
Borrelia Infections (MeSH)

IT Chemicals & Biochemicals
outer surface lipoprotein; ***VmpA***

ORGN . . .

Notes
Animals, Birds, Chordates, Nonhuman Vertebrates, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia anserina
Borrelia turicatae

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 41 OF 87 LIFESCI COPYRIGHT 2009 CSA on STN

AN 1999:65969 LIFESCI <<LOGINID::20090609>>

TI Specific antibodies reactive with the 22-kilodalton major outer surface protein of ***Borrelia*** anserina Ni-NL protect chicks from infection

AU Sambri, V.; Marangoni, A.; Olmo, A.; Storni, E.; Montagnani, M.; Fabbi, M.; Cevenini, R.*

CS Section of Microbiology, DMCSS, University of Bologna, St. Orsola Hospital, via Massarenti 9, 40138 Bologna, Italy; E-mail: cevenini@med.unibo.it

SO Infection and Immunity [Infect. Immun.], (19990500) vol. 65, no. 5, pp. 2633-2637.
ISSN: 0019-9567.

DT Journal

FS J

LA English

SL English

AB An outer surface lipoprotein of 22 kDa was identified in the avian pathogen ***Borrelia*** anserina Ni-NL by using antibody preparations reactive with bacterial surface-exposed proteins. Amino acid sequence analysis of the 22-kDa protein demonstrated 90% identity with ***VmpA*** of B. turicatae, suggesting that the protein belongs to the family of 20-kDa outer surface proteins of the genus ***Borrelia*** . All of the 60 chicks intramuscularly treated with antibodies specifically reacting

with the 22-kDa protein and infected with strain Ni-NL were completely protected from infection, since no spirochetemia was detected, and from death. Control chicks were treated with immune sera raised against apathogenic strain B. anserina Es, which expresses a prominent 20-kDa polypeptide that is also a member of the ***Vmp*** family but does not cross-react immunologically with the 22-kDa protein of the Ni-NL strain. These animals, infected with B. anserina Ni-NL, showed a high degree of spirochetemia 10 days after infection, and all died between 14 and 21 days after infection. The results showed that the 22-kDa surface protein of B. anserina Ni-NL is a determinant of the pathogenic potential of the strain and also confirmed that only strain-specific antibodies are protective against B. anserina infection.

TI Specific antibodies reactive with the 22-kilodalton major outer surface protein of ***Borrelia*** anserina Ni-NL protect chicks from infection

AB An outer surface lipoprotein of 22 kDa was identified in the avian pathogen ***Borrelia*** anserina Ni-NL by using antibody preparations reactive with bacterial surface-exposed proteins. Amino acid sequence analysis of the 22-kDa protein demonstrated 90% identity with ***VmpA*** of B. turicatae, suggesting that the protein belongs to the family of 20-kDa outer surface proteins of the genus ***Borrelia*** . All of the 60 chicks intramuscularly treated with antibodies specifically reacting with the 22-kDa protein and infected with strain Ni-NL. . . raised against apathogenic strain B. anserina Es, which expresses a prominent 20-kDa polypeptide that is also a member of the ***Vmp*** family but does not cross-react immunologically with the 22-kDa protein of the Ni-NL strain. These animals, infected with B. anserina. . .

UT Outer membranes; Lipoproteins; Antibodies; Immunization (passive); Antigenic determinants; 22kDa protein; ***VmpA*** protein; ***Borrelia*** anserina; ***Borrelia*** turicatae

L4 ANSWER 42 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 25

AN 1999:342464 BIOSIS <<LOGINID::20090609>>

DN PREV199900342464

TI The extended promoters for two outer membrane lipoprotein genes of ***Borrelia*** spp. uniquely include a T-rich region.

AU Sohaskey, Charles D.; Zuckert, Wolfram R.; Barbour, Alan G. [Reprint author]

CS Departments of Microbiology and Molecular Genetics and Medicine, University of California Irvine, B240 Med Sci I, Irvine, CA, 92697 4025, USA

SO Molecular Microbiology, (July, 1999) Vol. 33, No. 1, pp. 41-51. print. CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

ED Entered STN: 24 Aug 1999
Last Updated on STN: 24 Aug 1999

AB OspA and B proteins of ***Borrelia*** burgdorferi and ***Vmp*** proteins of ***Borrelia*** hermsii are abundant outer membrane lipoproteins, whose expression varies with the environment. The genes for these proteins have the '-35' and '-10' elements of a sigma70-type promoter. Deletions of the promoters for these genes were analysed with a chloramphenicol acetyltransferase (CAT) reporter gene and plasmid constructs that were stably maintained in Escherichia coli or transiently transfected into B. burgdorferi. Reporter expression was measured as susceptibility of transformed E. coli cells to chloramphenicol and the CAT activity of E. coli and B. burgdorferi lysates in vitro. Presence of the

'-10' element was essential for full activity in both B. burgdorferi and E. coli. Upstream of the '-35' elements of the ospAB and ***vmp*** promoters were tracts with Ts in 16 of 20 positions for B. burgdorferi and 18 of 20 positions for B. hermsii. Deletion of the T-rich region from the ospAB or ***vmp*** promoter caused a greater reduction of CAT activity in B. burgdorferi than in E. coli. The findings indicate that ospAB and ***vmp*** promoters are extended promoters with two parts: (i) a core region containing typical '-35' and '-10' elements and (ii) a unique T-rich region.

TI The extended promoters for two outer membrane lipoprotein genes of ***Borrelia*** spp. uniquely include a T-rich region.

AB OspA and B proteins of ***Borrelia*** burgdorferi and ***Vmp*** proteins of ***Borrelia*** hermsii are abundant outer membrane lipoproteins, whose expression varies with the environment. The genes for these proteins have the '-35'. . . essential for full activity in both B. burgdorferi and E. coli. Upstream of the '-35' elements of the ospAB and ***vmp*** promoters were tracts with Ts in 16 of 20 positions for B. burgdorferi and 18 of 20 positions for B. hermsii. Deletion of the T-rich region from the ospAB or ***vmp*** promoter caused a greater reduction of CAT activity in B. burgdorferi than in E. coli. The findings indicate that ospAB and ***vmp*** promoters are extended promoters with two parts: (i) a core region containing typical '-35' and '-10' elements and (ii) a. . .

IT . . .
and Molecular Biophysics)

IT Chemicals & Biochemicals
enzymes; outer membrane lipoprotein genes; outer membrane lipoproteins; outer membrane proteins; plasmids; proteins; ***Borrelia*** ospAB gene; ***Borrelia*** ***vmp*** gene

ORGN . . .
Escherichia coli
Taxa Notes
Bacteria, Eubacteria, Microorganisms

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia spp.
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 43 OF 87 SCISEARCH COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 1999:121219 SCISEARCH <<LOGINID::20090609>>

GA The Genuine Article (R) Number: 165HE

TI Antigenic variation in Lyme disease ***borreliae*** by promiscuous recombination of ***VMP*** -like sequence cassettes (vol 89, pg 275, 1997)

AU Zhang J R (Reprint)

CS Univ Texas, Sch Med, Dept Pathol & Lab Med, Houston, TX 77030 USA (Reprint)

AU Hardham J M; Barbour A G; Norris S J

CS Univ Texas, Sch Med, Dept Microbiol & Mol Genet, Houston, TX 77030 USA; Univ Calif Irvine, Coll Med, Dept Microbiol & Mol Genet, Irvine, CA 92697 USA

CYA USA

SO CELL, (5 FEB 1999) Vol. 96, No. 3, pp. U23-U23.
ISSN: 0092-8674.
PB CELL PRESS, 1100 MASSACHUSETTES AVE,, CAMBRIDGE, MA 02138 USA.
DT Errata; Journal
LA English
REC Reference Count: 1
ED Entered STN: 1999
Last Updated on STN: 1999
TI Antigenic variation in Lyme disease ***borreliae*** by promiscuous recombination of ***VMP*** -like sequence cassettes (vol 89, pg 275, 1997)

L4 ANSWER 44 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1999:123920 CAPLUS <<LOGINID::20090609>>
TI Antigenic variation in lyme disease ***borreliae*** by promiscuous recombination of ***VMP*** -like sequence cassettes
AU Anon.
SO Cell (Cambridge, Massachusetts) (1999), 96(3), no pp. Given
CODEN: CELLB5; ISSN: 0092-8674
PB Cell Press
DT Journal; Errata
LA English
AB Unavailable
TI Antigenic variation in lyme disease ***borreliae*** by promiscuous recombination of ***VMP*** -like sequence cassettes

L4 ANSWER 45 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 26
AN 1998:393355 BIOSIS <<LOGINID::20090609>>
DN PREV199800393355
TI Genetic variation of the ***Borrelia*** burgdorferi gene vlsE involves cassette-specific, segmental gene conversion.
AU Zhang, Jing-Ren; Norris, Steven J. [Reprint author]
CS Dep. Pathol. Lab. Med., Univ. Tex. Med. Sch., 6431 Fannin, Houston, TX 77030, USA
SO Infection and Immunity, (Aug., 1998) Vol. 66, No. 8, pp. 3698-3704. print.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 10 Sep 1998
Last Updated on STN: 10 Sep 1998
AB The Lyme disease spirochete ***Borrelia*** burgdorferi possesses 15 silent ***vls*** cassettes and a ***vls*** expression site (vlsE) encoding a surface-exposed lipoprotein. Segments of the silent ***vls*** cassettes have been shown to recombine with the vlsE cassette region in the mammalian host, resulting in combinatorial antigenic variation. Despite promiscuous recombination within the vlsE cassette region, the 5' and 3' coding sequences of vlsE that flank the cassette region are not subject to sequence variation during these recombination events. The segments of the silent ***vls*** cassettes recombine in the vlsE cassette region through a unidirectional process such that the sequence and organization of the silent ***vls*** loci are not affected. As a result of recombination, the previously expressed segments are replaced by incoming segments and apparently degraded. These results provide evidence for a gene conversion mechanism in VlsE antigenic variation.
TI Genetic variation of the ***Borrelia*** burgdorferi gene vlsE involves

cassette-specific, segmental gene conversion.

AB The Lyme disease spirochete ***Borrelia*** burgdorferi possesses 15 silent ***vls*** cassettes and a ***vls*** expression site (vlsE) encoding a surface-exposed lipoprotein. Segments of the silent ***vls*** cassettes have been shown to recombine with the vlsE cassette region in the mammalian host, resulting in combinatorial antigenic variation.. . . that flank the cassette region are not subject to sequence variation during these recombination events. The segments of the silent ***vls*** cassettes recombine in the vlsE cassette region through a unidirectional process such that the sequence and organization of the silent ***vls*** loci are not affected. As a result of recombination, the previously expressed segments are replaced by incoming segments and apparently. . .

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia -burgdorferi
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 46 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 27

AN 1998:393354 BIOSIS <<LOGINID::20090609>>

DN PREV199800393354

TI Kinetics and in vivo induction of genetic variation of vlsE in ***Borrelia*** burgdorferi.

AU Zhang, Jing-Ren; Norris, Steven J. [Reprint author]

CS Dep. Pathol. Lab. Med., Univ. Tex. Med. Sch., 6431 Fannin, Houston, TX 77030, USA

SO Infection and Immunity, (Aug., 1998) Vol. 66, No. 8, pp. 3689-3697. print. CODEN: INFIBR. ISSN: 0019-9567.

DT Article

LA English

ED Entered STN: 10 Sep 1998
Last Updated on STN: 10 Sep 1998

AB The Lyme disease agent, ***Borrelia*** burgdorferi, is able to persistently infect humans and animals for months or years in the presence of an active immune response. It is not known how the organisms survive immune attack in the mammalian host. vlsE, a gene localized near one end of linear plasmid lp28-1 and encoding a surface-exposed lipoprotein in B. burgdorferi B31, was shown recently to undergo extensive genetic and antigenic variation within 28 days of initial infection in C3H/HeN mice. In this study, we examined the kinetics of vlsE sequence variation in C3H/HeN mice at 4, 7, 14, 21, and 28 days and at 7 and 12 months postinfection. Sequence changes were detected by PCR amplification and sequence analysis as early as 4 days postinfection and accumulated progressively in both C3H/HeN and CB-17 severe combined immunodeficient (SCID) mice throughout the course of infection. The sequence changes were consistent with sequential recombination of segments from multiple silent ***vls*** cassette sites into the vlsE expression site. No vlsE sequence changes were detected in organisms cultured in vitro for up to 84 days. These results indicate that vlsE recombination is induced by a factor(s) present in the mammalian host, independent of adaptive immune responses. The possible inducing conditions appear to be present in various tissue sites because isolates from multiple tissues showed similar

degrees of sequence variation. The rate of accumulation of predicted amino acid changes was higher in the immunologically intact C3H/HeN mice than in SCID mice, a finding consistent with immune selection of VlsE variants.

TI Kinetics and in vivo induction of genetic variation of vlsE in ***Borrelia*** burgdorferi.

AB The Lyme disease agent, ***Borrelia*** burgdorferi, is able to persistently infect humans and animals for months or years in the presence of an active immune. . . (SCID) mice throughout the course of infection. The sequence changes were consistent with sequential recombination of segments from multiple silent ***vls*** cassette sites into the vlsE expression site. No vlsE sequence changes were detected in organisms cultured in vitro for up. . .

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia -burgdorferi

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 47 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 28

AN 1998:352289 BIOSIS <<LOGINID::20090609>>

DN PREV199800352289

TI Bloodstream-versus tick-associated variants of a relapsing fever bacterium.

AU Schwan, Tom G. [Reprint author]; Hinnebusch, B. Joseph

CS Lab. Microbial Structure Function, Rocky Mountain Laboratories, Natl. Inst. Allergy Infectious Diseases, Natl. Inst. Health, Hamilton, MT 59840, USA

SO Science (Washington D C), (June 19, 1998) Vol. 280, No. 5371, pp. 1938-1940. print.
CODEN: SCIEAS. ISSN: 0036-8075.

DT Article

LA English

ED Entered STN: 13 Aug 1998
Last Updated on STN: 13 Aug 1998

AB The relapsing fever spirochete, ***Borrelia*** hermsii, alternates infections between a mammal and a tick vector. Whether the spirochete changes phenotypically in the different hosts was examined by allowing the tick vector Ornithodoros hermsi to feed on mice infected with serotype 7 or serotype 8 of B. hermsii. Upon infection of ticks, the spirochetal serotype-specific variable major proteins (***Vmps***) 7 and 8 became undetectable and were replaced by ***Vmp33*** . This switch from a bloodstream- to tick-associated phenotype could be induced in culture by a decrease in temperature. After tick-bite transmission back to mice, the process was reversed and the spirochetes resumed expression of the same ***Vmp*** present in the previous infectious blood meal.

AB The relapsing fever spirochete, ***Borrelia*** hermsii, alternates infections between a mammal and a tick vector. Whether the spirochete changes phenotypically in the different hosts was. . . infected with serotype 7 or serotype 8 of B. hermsii. Upon infection of ticks, the spirochetal serotype-specific variable major proteins (***Vmps***) 7

and 8 became undetectable and were replaced by ***Vmp33*** . This switch from a bloodstream- to tick-associated phenotype could be induced in culture by a decrease in temperature. After tick-bite transmission back to mice, the process was reversed and the spirochetes resumed expression of the same ***Vmp*** present in the previous infectious blood meal.

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia -hermsii: bloodstream variant, pathogen, serovar-7, relapsing fever spirochete, serovar-8, tick-associated variant, tick bite transmission

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 48 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 29
AN 1998:787140 CAPLUS <<LOGINID::20090609>>
DN 130:152425
TI Variable major lipoprotein is a principal TNF-inducing factor of louse-borne relapsing fever
AU Vidal, Vincent; Scragg, Ian G.; Cutler, Sally J.; Rockett, Kirk A.; Rekade, Daniel; Warrell, David A.; Wright, David J. M.; Kwiatkowski, Dominic
CS University Department of Pediatrics, Oxford University, UK
SO Nature Medicine (New York) (1998), 4(12), 1416-1420
CODEN: NAMEFI; ISSN: 1078-8956
PB Nature America
DT Journal
LA English
AB Massive release of tumor necrosis factor is responsible for the potentially fatal Jarisch-Herxheimer reaction that follows antibiotic treatment of relapsing fever due to ***Borrelia*** recurrentis. The authors have undertaken the quant. purifn. of the components of B. recurrentis that stimulate human monocytes to produce tumor necrosis factor. The authors show that the predominant factor inducing tumor necrosis factor is a variable lipoprotein homologous to the variable major protein of B. hermsii. The authors found antibodies to different forms of variable major protein in two patients with louse-borne relapsing fever. The three purified variable major proteins studied here differ in their ability to induce tumor necrosis factor prodn., which may partly explain the variable clin. severity of ***borrelial*** infection. These results may be of considerable relevance for the pathogenesis of Lyme disease and other forms of human ***borreliosis*** .
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
AB . . . tumor necrosis factor is responsible for the potentially fatal Jarisch-Herxheimer reaction that follows antibiotic treatment of relapsing fever due to ***Borrelia*** recurrentis. The authors have undertaken the quant. purifn. of the components of B. recurrentis that stimulate human monocytes to produce. . . here differ in their ability to induce tumor necrosis factor prodn., which may partly explain the variable clin. severity of ***borrelial*** infection. These results may be of considerable relevance for the pathogenesis of Lyme disease and other

forms of human ***borreliosis*** .
ST ***vmpA1*** lipoprotein tumor necrosis factor louse borne relapsing fever; sequence variable major protein ***vmpA1*** gene ***Borrelia***
IT Disease, animal
(Jarisch-Herxheimer reaction; variable major lipoprotein A1 of ***Borrelia*** recurrentis sequence and as principal tumor necrosis factor-inducing factor of louse-borne relapsing fever in humans in relation to)
IT Lipoproteins
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(***VmpA1*** (variable major protein A1); variable major lipoprotein A1 of ***Borrelia*** recurrentis sequence and as principal tumor necrosis factor-inducing factor of louse-borne relapsing fever in humans)
IT Fever and Hyperthermia
(louse-borne relapsing; variable major lipoprotein A1 of ***Borrelia*** recurrentis sequence and as principal tumor necrosis factor-inducing factor of louse-borne relapsing fever in humans)
IT DNA sequences
(of variable major protein A1 gene ***vmpA1*** of ***Borrelia*** recurrentis)
IT Protein sequences
(of variable major protein A1 of ***Borrelia*** recurrentis)
IT ***Borrelia*** recurrentis
(variable major lipoprotein A1 of ***Borrelia*** recurrentis sequence and as principal tumor necrosis factor-inducing factor of louse-borne relapsing fever in humans)
IT Tumor necrosis factors
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(variable major lipoprotein A1 of ***Borrelia*** recurrentis sequence and as principal tumor necrosis factor-inducing factor of louse-borne relapsing fever in humans)
IT Gene, microbial
RL: PRP (Properties)
(***vmpA1*** ; variable major lipoprotein A1 of ***Borrelia*** recurrentis sequence and as principal tumor necrosis factor-inducing factor of louse-borne relapsing fever in humans)
IT 206631-77-8, GenBank AJ224157
RL: PRP (Properties)
(nucleotide sequence; variable major lipoprotein A1 of ***Borrelia*** recurrentis sequence and as principal tumor necrosis factor-inducing factor of louse-borne relapsing fever in humans)

L4 ANSWER 49 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 30
AN 1998:120628 BIOSIS <<LOGINID::20090609>>
DN PREV199800120628
TI Population structure of the relapsing fever spirochete ***Borrelia*** hermsii as indicated by polymorphism of two multigene families that encode immunogenic outer surface lipoproteins.
AU Hinnebusch, B. Joseph [Reprint author]; Barbour, Alan G.; Restrepo, Blanca I.; Schwan, Tom G.
CS Lab. Microbial Structure Function, Rocky Mountain Lab., Natl. Inst.

Allergy Infectious Diseases, Natl. Inst. Health, 903 S. 4th St., Hamilton, MT 59840, USA
SO Infection and Immunity, (Feb., 1998) Vol. 66, No. 2, pp. 432-440. print. CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
ED Entered STN: 5 Mar 1998
Last Updated on STN: 5 Mar 1998
AB The tick-borne relapsing fever spirochete ***Borrelia*** hermsii evades the mammalian immune system by periodically switching expression among members of two multigene families that encode immunogenic, antigenically distinct outer surface proteins. The type strain, B. hermsii HS1, has at least 40 complete genes and pseudogenes that participate in this multiphasic antigenic variation. Originally termed ***vmp*** (for variable major protein) genes, they have been reclassified as vsp (for variable small protein) and vlp (for variable large protein) genes, based on size and amino acid sequence similarities. To date, antigenic variation in B. hermsii has been studied only in the type strain, HS1. Nucleotide sequence comparisons of 23 B. hermsii HS1 genes revealed five distinct groups, the vsp gene family and four subfamilies of vlp genes. We used PCR with family- and subfamily-specific primers, followed by restriction fragment length polymorphism analysis, to compare the vsp and vlp repertoires of HS1 and seven other B. hermsii isolates from Washington, Idaho, and California. This analysis, together with pulsed-field gel electrophoresis genome profiles, revealed that the eight isolates formed three distinct groups, which likely represent clonal lineages. Members of the three groups coexisted in the same geographic area, but they could also be isolated across large geographical distances. This population structure may result from immune selection by the host, as has been proposed for other pathogens with polymorphic antigens.
TI Population structure of the relapsing fever spirochete ***Borrelia*** hermsii as indicated by polymorphism of two multigene families that encode immunogenic outer surface lipoproteins.
AB The tick-borne relapsing fever spirochete ***Borrelia*** hermsii evades the mammalian immune system by periodically switching expression among members of two multigene families that encode immunogenic, antigenically. . . B. hermsii HS1, has at least 40 complete genes and pseudogenes that participate in this multiphasic antigenic variation. Originally termed ***vmp*** (for variable major protein) genes, they have been reclassified as vsp (for variable small protein) and vlp (for variable large. . .
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia -hermsii: tick-borne relapsing fever spirochete
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 50 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1998:416557 BIOSIS <<LOGINID::20090609>>
DN PREV199800416557
TI Human tissue culture cells induce the ***Vmp*** -like outer membrane protein, VlsE, in ***Borrelia*** burgdorferi.
AU Frye, J. G.; Hudson, C. R.; Gherardini, F. C.

CS Univ. Ga., Athens, GA, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (1998) Vol. 98, pp. 222. print.
Meeting Info.: 98th General Meeting of the American Society for Microbiology. Atlanta, Georgia, USA. May 17-21, 1998. American Society for Microbiology.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 2 Oct 1998
Last Updated on STN: 2 Oct 1998
TI Human tissue culture cells induce the ***Vmp*** -like outer membrane protein, VlsE, in ***Borrelia*** burgdorferi.
IT . . .
Bacteriology; Genetics
IT Diseases
Lyme disease: bacterial disease
Lyme Disease (MeSH)
IT Chemicals & Biochemicals
mRNA [messenger RNA]; DNA; RNA; VlsE: ***Vmp*** -like outer membrane protein
ORGN . . .
Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia -burgdorferi: pathogen
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 51 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 31
AN 1998:213424 BIOSIS <<LOGINID::20090609>>
DN PREV199800213424
TI Genetic and immunological analyses of VIs (***VMP*** -like sequences) of ***Borrelia*** burgdorferi.
AU Kawabata, Hiroki; Myouga, Fumiyoshi; Inagaki, Yoshishige; Murai, Noriyuki; Watanabe, Haruo [Reprint author]
CS Dep. Bacteriol., Natl. Inst. Infect. Dis., 1-23-1 Toyama, Shinjyuku-ku, Tokyo 162, Japan
SO Microbial Pathogenesis, (March, 1998) Vol. 24, No. 3, pp. 155-166. print.
CODEN: MIPAEV. ISSN: 0882-4010.
DT Article
LA English
ED Entered STN: 11 May 1998
Last Updated on STN: 11 May 1998
AB DNA fragments containing the ***VMP*** -like sequence (***Vls***) were cloned from ***Borrelia*** burgdorferi strain 297. Analyses by PCR, PFGE, and Southern hybridization revealed that the ***Vls*** sequences existed in multi-copies on the 20-kb ***borrelial*** plasmid, but not on chromosomes or other plasmids. One ***Vls*** unit of the strain 297 was about 669 bases, and predicted peptides length was

223 amino acids. Homologues of the ***Vls*** fragment were detected in three B. burgdorferi strains, a B. garinii strain 20047, and a B. afzelii strain P/Gau. A recombinant VlsII protein prepared in Escherichia coli strain JM109 reacted with antibodies that existed in three of five patients, by immunoblotting. These results suggested that the ***Vls*** of B. burgdorferi is expressed in Lyme disease patients.

TI Genetic and immunological analyses of VIs (***VMP*** -like sequences) of ***Borrelia*** burgdorferi.

AB DNA fragments containing the ***VMP*** -like sequence (***Vls***) were cloned from ***Borrelia*** burgdorferi strain 297. Analyses by PCR, PFGE, and Southern hybridization revealed that the ***Vls*** sequences existed in multi-copies on the 20-kb ***borrelial*** plasmid, but not on chromosomes or other plasmids. One ***Vls*** unit of the strain 297 was about 669 bases, and predicted peptides length was 223 amino acids. Homologues of the ***Vls*** fragment were detected in three B. burgdorferi strains, a B. garinii strain 20047, and a B. afzelii strain P/Gau. A. . . coli strain JM109 reacted with antibodies that existed in three of five patients, by immunoblotting. These results suggested that the ***Vls*** of B. burgdorferi is expressed in Lyme disease patients.

IT . . .

Diseases

Lyme disease: bacterial disease

Lyme Disease (MeSH)

IT Chemicals & Biochemicals

ospC gene; outer surface protein C; variable major protein; ***vls*** gene

ORGN Classifier

Spirochaetaceae 06112

Super Taxa

Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name

Borrelia -burgdorferi: pathogen

Borrelia -hermsii: pathogen

Taxa Notes

Bacteria, Eubacteria, Microorganisms

L4 ANSWER 52 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN

AN 1998:152421 CAPLUS <<LOGINID::20090609>>

DN 128:201751

OREF 128:39807a,39810a

TI Antigenic variation in Lyme disease spirochetes by segmental recombination of ***vmp*** -like sequence cassettes

AU Zhang, Jing-Ren

CS Health Science Center, Univ. of Texas, Houston, TX, USA

SO (1997) 126 pp. Avail.: UMI, Order No. DA9813074

From: Diss. Abstr. Int., B 1998, 58(10), 5258

DT Dissertation

LA English

AB Unavailable

TI Antigenic variation in Lyme disease spirochetes by segmental recombination of ***vmp*** -like sequence cassettes

ST antigenic variation Lyme disease spirochete recombination; ***vmp*** cassette sequence segmental recombination ***Borrelia***

IT Antigenic variation

Borrelia burgdorferi

Recombination, genetic

(antigenic variation in Lyme disease spirochetes by segmental recombination of ***vmp*** -like sequence cassettes)

IT Antigens
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(antigenic variation in Lyme disease spirochetes by segmental recombination of ***vmp*** -like sequence cassettes)

IT Gene, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(***vmp*** ; antigenic variation in Lyme disease spirochetes by segmental recombination of ***vmp*** -like sequence cassettes)

L4 ANSWER 53 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:579836 CAPLUS <<LOGINID::20090609>>
DN 127:189742
OREF 127:36809a,36812a
TI ***Vmp*** -like sequences of pathogenic ***Borrelia***
IN Norris, Steven J.; Zhang, Jing-ren; Hardham, John M.; Howell, Jerrilyn K.; Barbour, Alan G.; Weinstock, George M.
PA Board of Regents, the University of Texas System, USA; Norris, Steven J.; Zhang, Jing-Ren; Hardham, John M.; Howell, Jerrilyn K.; Barbour, Alan G.; Weinstock, George M.
SO PCT Int. Appl., 130 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9731123	A1	19970828	WO 1997-US2952	19970220
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9721915	A	19970910	AU 1997-21915	19970220
	EP 894143	A1	19990203	EP 1997-914794	19970220
	EP 894143	B1	20050810		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	AT 301716	T	20050815	AT 1997-914794	19970220
	EP 1589109	A2	20051026	EP 2005-10338	19970220
	EP 1589109	A3	20051116		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	US 6437116	B1	20020820	US 1999-125619	19990127
	US 20030092903	A1	20030515	US 2002-143024	20020731
	US 6740744	B2	20040525		
	US 20030060618	A1	20030327	US 2002-222162	20020816
	US 6878816	B2	20050412		
	US 20040044192	A1	20040304	US 2002-222566	20020816
	US 6719983	B2	20040413		
	US 20040214225	A1	20041028	US 2004-852555	20040524
	US 7135176	B2	20061114		

US 20070117970 A1 20070524 US 2006-501166 20060807
PRAI US 1996-12028P P 19960221
EP 1997-914794 A3 19970220
WO 1997-US2952 W 19970220
US 1999-125619 A3 19990127
US 2002-143024 A3 20020731
US 2002-222162 A3 20020816
US 2004-852555 A3 20040524
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the DNA and amino acid sequences to the prodn. of polypeptides as antigens for immunoprophylaxis, immunotherapy, and immunodiagnosis. Also disclosed are the use of the nucleic acid sequences as probes or primers for the detection of organisms causing Lyme disease, relapsing fever, or related disorders, and kits designed to facilitate methods of using the described polypeptides, DNA segments and antibodies.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI ***Vmp*** -like sequences of pathogenic ***Borrelia***
AB The present invention relates to DNA sequences encoding ***Vmp*** -like polypeptides of pathogenic ***Borrelia*** , the use of the DNA sequences in recombinant vectors to express polypeptides, the encoded amino acid sequences, application of the. . .
ST variable major protein gene ***Borrelia***
IT ***Borrelia*** burgdorferi
(***Vmp*** -like sequences of pathogenic ***Borrelia***)
IT Proteins, specific or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(gene vlsE; ***Vmp*** -like sequences of pathogenic ***Borrelia***)
IT 189614-97-9, DNA (***Borrelia*** burgdorferi strain B31 clone 5A3 gene vlsE plus flanks)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(***Vmp*** -like sequences of pathogenic ***Borrelia***)
IT 189833-73-6, Protein (***Borrelia*** burgdorferi strain B31 clone 5A3 gene vlsE)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(***Vmp*** -like sequences of pathogenic ***Borrelia***)

L4 ANSWER 54 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 32
AN 1997:391165 BIOSIS <<LOGINID::20090609>>
DN PREV199799690368
TI Immunologic and genetic analyses of ***VmpA*** of a neurotropic strain of ***Borrelia*** turicatae.
AU Cadavid, Diego; Pennington, Pamela M.; Kerentseva, Tatiana A.; Bergstrom, Sven; Barbour, Alan G. [Reprint author]
CS Dep. Microbiol. Molecular Genetics, Univ. California Irvine, Irvine, CA 92697-4025, USA
SO Infection and Immunity, (1997) Vol. 65, No. 8, pp. 3352-3360.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article

LA English
ED Entered STN: 10 Sep 1997
Last Updated on STN: 10 Sep 1997
AB In mice infected with serotype A but not serotype B of the relapsing fever spirochete ***Borrelia*** turicatae, early invasion of the brain occurs. Serotypes A and B are further distinguished by the abundant surface protein they produce: ***VmpA*** and ***VmpB*** , respectively. Western blotting with monoclonal antibodies, one-dimensional peptide mapping, and partial amino acid sequencing demonstrated regions of the ***VmpA*** protein that differed from ***VmpB*** . Oligonucleotide primers based on the partial amino acid sequences of unique regions were used to amplify a portion of the ***VmpA*** gene (***vmpA***) by PCR, and the product was used as a probe in Southern blot and Northern blot analyses. These experiments showed that (i) expression of the ***vmpA*** sequence was determined at the level of transcription and (ii) the ***vmpA*** sequence was in two locations in serotype A and one location in serotype B. The ***vmpA*** gene at the expression-linked locus of serotype A was cloned and sequenced. An open reading frame would encode a polypeptide of 214 amino acids. The polypeptide expressed by Escherichia coli was bound by VmA-specific but not ***VmpB*** -specific antibody. Primer extension analysis identified a consensus sigma-70-type promoter for ***vmpA*** at the expression locus. Phylogenetic analysis revealed that ***VmpA*** is homologous to small ***Vmp*** (Vsp) proteins of B. hermsii and to OspC proteins of B. burgdorferi. These findings indicate that a function of the Vsp-OspC family of proteins of ***Borrelia*** spp. may be differential localization in organs, including the brain, during infection.
TI Immunologic and genetic analyses of ***VmpA*** of a neurotropic strain of ***Borrelia*** turicatae.
AB In mice infected with serotype A but not serotype B of the relapsing fever spirochete ***Borrelia*** turicatae, early invasion of the brain occurs. Serotypes A and B are further distinguished by the abundant surface protein they produce: ***VmpA*** and ***VmpB*** , respectively. Western blotting with monoclonal antibodies, one-dimensional peptide mapping, and partial amino acid sequencing demonstrated regions of the ***VmpA*** protein that differed from ***VmpB*** . Oligonucleotide primers based on the partial amino acid sequences of unique regions were used to amplify a portion of the ***VmpA*** gene (***vmpA***) by PCR, and the product was used as a probe in Southern blot and Northern blot analyses. These experiments showed that (i) expression of the ***vmpA*** sequence was determined at the level of transcription and (ii) the ***vmpA*** sequence was in two locations in serotype A and one location in serotype B. The ***vmpA*** gene at the expression-linked locus of serotype A was cloned and sequenced. An open reading frame would encode a polypeptide of 214 amino acids. The polypeptide expressed by Escherichia coli was bound by VmA-specific but not ***VmpB*** -specific antibody. Primer extension analysis identified a consensus sigma-70-type promoter for ***vmpA*** at the expression locus. Phylogenetic analysis revealed that ***VmpA*** is homologous to small ***Vmp*** (Vsp) proteins of B. hermsii and to OspC proteins of B. burgdorferi. These findings indicate that a function of the Vsp-OspC family of proteins of ***Borrelia*** spp. may be differential localization in organs, including the brain, during infection.
IT . . .
METHOD; BACTERIAL DISEASE; BRAIN INFECTION; INFECTION; MOLECULAR

GENETICS; NCBI DATABANK; NERVOUS SYSTEM DISEASE; POLYMERASE CHAIN REACTION; SEROVAR-A; SEROVAR-B; STRUCTURE; U85413; ***VMPA*** GENE

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia turicatae
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 55 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 33
AN 1997:225972 BIOSIS <<LOGINID::20090609>>
DN PREV199799517688
TI Antigenic variation in Lyme disease ***Borreliae*** by promiscuous recombination of ***VMP*** -like sequence cassettes.
AU Zhang, Jing-Ren [Reprint author]; Hardham, John M.; Barbour, Alan G.; Norris, Steven J.
CS Dep. Pathol., Univ. Texas Med. Sch. Houston, Houston, TX 77030, USA
SO Cell, (1997) Vol. 89, No. 2, pp. 275-285.
CODEN: CELLB5. ISSN: 0092-8674.
DT Article
LA English
ED Entered STN: 22 May 1997
Last Updated on STN: 22 May 1997
AB We have identified and characterized an elaborate genetic system in the Lyme disease spirochete ***Borrelia*** burgdorferi that promotes extensive antigenic variation of a surface-exposed lipoprotein, VlsE. A 28 kb linear plasmid of B. burgdorferi B31 (lp28-1) was found to contain a ***vmp*** -like sequence (***vls***) locus that closely resembles the variable major protein (***vmp***) system for antigenic variation of relapsing fever organisms. Portions of several of the 15 nonexpressed (silent) ***vls*** cassette sequences located upstream of vlsE recombined into the central vlsE cassette region during infection of C3H/HeN mice, resulting in antigenic variation of the expressed lipoprotein. This combinatorial variation could potentially produce millions of antigenic variants in the mammalian host.
TI Antigenic variation in Lyme disease ***Borreliae*** by promiscuous recombination of ***VMP*** -like sequence cassettes.
AB We have identified and characterized an elaborate genetic system in the Lyme disease spirochete ***Borrelia*** burgdorferi that promotes extensive antigenic variation of a surface-exposed lipoprotein, VlsE. A 28 kb linear plasmid of B. burgdorferi B31 (lp28-1) was found to contain a ***vmp*** -like sequence (***vls***) locus that closely resembles the variable major protein (***vmp***) system for antigenic variation of relapsing fever organisms. Portions of several of the 15 nonexpressed (silent) ***vls*** cassette sequences located upstream of vlsE recombined into the central vlsE cassette region during infection of C3H/HeN mice, resulting in. . .
IT Miscellaneous Descriptors
ANTIGENIC VARIATION; BACTERIAL DISEASE; COMBINATORIAL VARIATION; C3H/HEN; INFECTION; LYME DISEASE; MOLECULAR GENETICS; PATHOGEN; PROMISCUOUS RECOMBINATION; SURFACE-EXPOSED LIPOPROTEIN; VLSE; ***VMP*** -LIKE SEQUENCE CASSETTES

ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 56 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1997:282165 BIOSIS <<LOGINID::20090609>>
DN PREV199799581368
TI Antigenic variation in Lyme disease spirochetes by promiscuous recombination of ***vmp*** -like sequence cassettes.
AU Zhang, Jing-Ren [Reprint author]; Hardham, John M.; Barbour, Alan G.; Norris, Steven J.
CS Dep. Pathol. Lab. Med., Univ. Texas Med. Sch., Houston, TX, USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (1997) Vol. 97, No. 0, pp. 103.
Meeting Info.: 97th General Meeting of the American Society for Microbiology. Miami Beach, Florida, USA. May 4-8, 1997.
ISSN: 1060-2011.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 3 Jul 1997
Last Updated on STN: 3 Jul 1997
TI Antigenic variation in Lyme disease spirochetes by promiscuous recombination of ***vmp*** -like sequence cassettes.
ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 57 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 34
AN 2002:51422 BIOSIS <<LOGINID::20090609>>
DN PREV200200051422
TI Cloning and expression of soluble truncated variants of ***Borrelia*** OSPA, OSPB and ***VMP7*** .
AU Dunn, J. J. [Inventor]; Barbour, A. G. [Inventor]
CS Bellport, N.Y., USA
ASSIGNEE: ASSOCIATED UNIVERSITIES, INC.
PI US 5571718 19961105
SO Official Gazette of the United States Patent and Trademark Office Patents, (Nov. 5, 1996) Vol. 1192, No. 1, pp. 420. print.
CODEN: OGUPE7. ISSN: 0098-1133.

```
DT   Patent
LA   English
ED   Entered STN: 2 Jan 2002
     Last Updated on STN: 25 Feb 2002
TI   Cloning and expression of soluble truncated variants of   ***Borrelia***
     OSPA, OSPB and   ***VMP7***  .

L4   ANSWER 58 OF 87  CAPLUS  COPYRIGHT 2009 ACS on STN
AN   1996:583427  CAPLUS <<LOGINID::20090609>>
DN   125:266978
OREF 125:49633a,49636a
TI   Homology of variable major protein genes between   ***Borrelia***
     hermsii and   ***Borrelia***   miyamotoi. [Erratum to document cited in
     CA125:159805]
AU   Hamase, Akiko; Takahashi, Yukie; Nohgi, Keiko; Fukunaga, Masahito
CS   Laboratory of Molecular Microbiology, Faculty of Pharmacy and
     Pharmaceutical Sciences, Fukuyama University, Hiroshima, 729-02, Japan
SO   FEMS Microbiology Letters (1996), 143(2-3), 299
     CODEN: FMLED7; ISSN: 0378-1097
PB   Elsevier
DT   Journal
LA   English
AB   The errors were not reflected in the abstr. or the index entries.
TI   Homology of variable major protein genes between   ***Borrelia***
     hermsii and   ***Borrelia***   miyamotoi. [Erratum to document cited in
     CA125:159805]
ST   erratum   ***Borrelia***     ***vmp***   like gene DNA;   ***Borrelia***
       ***vmp***   like gene DNA erratum;   ***vmp***   like gene DNA sequence
     erratum; variable major protein sequence   ***Borrelia***   erratum
IT   Proteins, specific or class
     RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP
     (Properties); BIOL (Biological study); OCCU (Occurrence)
        (  ***VMP***   (variable major proteins); characterization of
          ***Borrelia***   miyamotoi   ***vmp***  -like genes from strains HT31
        and FR64b and   ***Borrelia***   hermsii and comparison of amino acid
        sequence to published   ***vmp***   proteins of   ***Borrelia***
        hermsii (Erratum))
IT    ***Borrelia***   hermsii
       ***Borrelia***   miyamotoi
     Deoxyribonucleic acid sequences
     Protein sequences
        (characterization of   ***Borrelia***   miyamotoi   ***vmp***  -like
        genes from strains HT31 and FR64b and   ***Borrelia***   hermsii and
        comparison of amino acid sequence to published   ***vmp***   proteins
        of   ***Borrelia***   hermsii (Erratum))
IT   Gene, microbial
     RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP
     (Properties); BIOL (Biological study); OCCU (Occurrence)
        (  ***vmp***  -like; characterization of   ***Borrelia***   miyamotoi
          ***vmp***  -like genes from strains HT31 and FR64b and
***Borrelia***
        hermsii and comparison of amino acid sequence to published   ***vmp***
        proteins of   ***Borrelia***   hermsii (Erratum))
IT   180291-11-6
     RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP
     (Properties); BIOL (Biological study); OCCU (Occurrence)
        (amino acid sequence; characterization of   ***Borrelia***   miyamotoi
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vmp -like genes from strains HT31 and FR64b and ***Borrelia*** hermsii and comparison of amino acid sequence to published ***vmp*** proteins of ***Borrelia*** hermsii (Erratum))

IT 180291-12-7 180308-88-7
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(characterization of ***Borrelia*** miyamotoi ***vmp*** -like genes from strains HT31 and FR64b and ***Borrelia*** hermsii and comparison of amino acid sequence to published ***vmp*** proteins of ***Borrelia*** hermsii (Erratum))

IT 180308-87-6
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; characterization of ***Borrelia*** miyamotoi ***vmp*** -like genes from strains HT31 and FR64b and ***Borrelia*** hermsii and comparison of amino acid sequence to published ***vmp*** proteins of ***Borrelia*** hermsii (Erratum))

L4 ANSWER 59 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 35
AN 1996:379860 BIOSIS <<LOGINID::20090609>>
DN PREV199699102216
TI Homology of variable major protein genes between ***Borrelia*** hermsii and ***Borrelia*** miyamotoi.
AU Hamase, Akiko; Takahashi, Yukie; Nohgi, Keiko; Fukunaga, Masahito [Reprint author]
CS Lab. Mol. Microbiol., Fac. Pharmacy Pharmaceutical Sci., Fukuyama Univ., Sanzo 985, Japan
SO FEMS Microbiology Letters, (1996) Vol. 140, No. 2-3, pp. 131-137.
CODEN: FMLED7. ISSN: 0378-1097.
DT Article
LA English
ED Entered STN: 26 Aug 1996
Last Updated on STN: 26 Aug 1996
AB Antigenic variation has been studied in detail for the etiological agent of relapsing fever, ***Borrelia*** hermsii. The variable major proteins (***vmps***) are found at its cell surface, enabling it to avoid the host's immune response. We have cloned and sequenced the ***vmp*** -gene (***vmp***)-like sequences from the ***Borrelia*** miyamotoi strains HT31 and FR64b and the deduced amino acid sequences were compared with the published ***vmp*** proteins ***vmp3*** , ***vmp24*** , and ***vmp33*** of B. hermsii. The sequences were aligned and revealed pairwise sequence identities ranging from 45 to 51%, and differences were scattered throughout the sequences. Southern hybridization using the cloned ***vmp*** -like sequence of strain HT31 as a probe suggested that the ump homologues reside on the linear plasmids of B. miyamotoi. The probe hybridized weakly with B. hermsii linear plasmids and restriction digests. These results suggest that B. miyamotoi has sequences resembling the ump genes in B. hermsii.
TI Homology of variable major protein genes between ***Borrelia*** hermsii and ***Borrelia*** miyamotoi.
AB Antigenic variation has been studied in detail for the etiological agent of relapsing fever, ***Borrelia*** hermsii. The variable major proteins (***vmps***) are found at its cell surface, enabling it to avoid the host's immune response. We have cloned and sequenced the

vmp -gene (***vmp***)-like sequences from the ***Borrelia*** miyamotoi strains HT31 and FR64b and the deduced amino acid sequences were compared with the published ***vmp*** proteins ***vmp3*** , ***vmp24*** , and ***vmp33*** of B. hermsii. The sequences were aligned and revealed pairwise sequence identities ranging from 45 to 51%, and differences were scattered throughout the sequences. Southern hybridization using the cloned ***vmp*** -like sequence of strain HT31 as a probe suggested that the ump homologues reside on the linear plasmids of B. miyamotoi.. . .

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia hermsii
Borrelia miyamotoi
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 60 OF 87 CABA COPYRIGHT 2009 CABI on STN
AN 97:98689 CABA <<LOGINID::20090609>>
DN 19970502811
TI The ***Borrelia*** turicatae murine model of Lyme disease
AU Barbour, A. G.
CS Department of Medicine (Infectious Disease) and Microbiology, University of Texas Health Science Center, San Antonio, TX 78284, USA.
SO Journal of Spirochetal and Tick-borne Diseases, (1996) Vol. 3, No. 1, pp. 62-66. 19 ref.
DT Journal
LA English
ED Entered STN: 16 Sep 1997
Last Updated on STN: 16 Sep 1997
AB ***Borrelia*** turicatae is an agent of relapsing fever. During relapsing fever, spirochaetes avoid the immune response of the host by a multiphasic antigenic variation. In B. hermsii, another agent of relapsing fever, the mechanism for the switch in antigens is a gene rearrangement, namely an interplasmidic gene conversion or an intraplasmidic deletion between direct repeats. In severe combined immunodeficiency (scid) mice, B. turicatae causes the constellation of arthritis, myocarditis, uveitis and a cranial nerve disorder. In this way, the infection in these mice is similar to Lyme disease. Moreover, B. turicatae invades and persists in the central nervous system of laboratory mice. The severity of illness, particularly the arthritis, and the entry into the brain appear to be determined by the small ***Vmp*** proteins of this species. These proteins are homologous to the polymorphic OspC proteins of B. burgdorferi, the agent of Lyme disease.
TI The ***Borrelia*** turicatae murine model of Lyme disease.
AB ***Borrelia*** turicatae is an agent of relapsing fever. During relapsing fever, spirochaetes avoid the immune response of the host by a. . . The severity of illness, particularly the arthritis, and the entry into the brain appear to be determined by the small ***Vmp*** proteins of this species. These proteins are homologous to the polymorphic OspC proteins of B. burgdorferi, the agent of Lyme. . .
BT ***Borrelia*** ; Spirochaetaceae; Spirochaetales; Gracilicutes; bacteria; prokaryotes; Muridae; rodents; mammals; vertebrates; Chordata; animals; small mammals
ORGN ***Borrelia*** hermsii; ***Borrelia*** burgdorferi;

Borrelia turicatae; mice

L4 ANSWER 61 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 36
AN 1995:320318 BIOSIS <<LOGINID::20090609>>
DN PREV199598334618
TI Evolution of the ***Borrelia*** burgdorferi outer surface protein OspC.
AU Theisen, Michael [Reprint author]; Borre, Martin; Mathiesen, Marianne J.; Mikkelsen, Bo; Lebech, Anne-Mette; Hansen, Klaus
CS Dep. Infection-Immunol., Statens Seruminstitut, Artillerivej 5, Copenhagen DK-2300, Denmark
SO Journal of Bacteriology, (1995) Vol. 177, No. 11, pp. 3036-3044. CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 30 Jul 1995
Last Updated on STN: 30 Jul 1995
AB The genes coding for outer surface protein OspC from 22 ***Borrelia*** burgdorferi strains isolated from patients with Lyme ***borreliosis*** were cloned and sequenced. For reference purposes, the 16S rRNA genes from 17 of these strains were sequenced after being cloned. The deduced OspC amino acid sequences were aligned with 12 published OspC sequences and revealed the presence of 48 conserved amino acids. On the basis of the alignment, OspC could be divided into an amino-terminal relatively conserved region and a relatively variable region in the central portion. The distance tree obtained divided the ospC sequences into three groups. The first group contained ospC alleles from all (n = 13) sensu stricto strains, the second group contained ospC alleles from seven ***Borrelia*** afzelii strains, and the third group contained ospC alleles from five B. afzelii and all (n = 9) ***Borrelia*** garinii strains. The ratio of the mean number of synonymous (d-S) and nonsynonymous (d-N) nucleotide substitutions per site calculated for B. burgdorferi sensu stricto, B. garinii, and B. afzelii ospC alleles suggested that the polymorphism of OspC is due to positive selection favoring diversity at the amino acid level in the relatively variable region. On the basis of the comparison of 16S rRNA gene sequences, ***Borrelia*** hermsii is more closely related to B. afzelii than to B. burgdorferi sensu stricto and B. garinii. In contrast, the phylogenetic tree obtained for the B. hermsii variable major protein, ***Vmp33*** , and 18 OspC amino acid sequences suggested that ***Vmp33*** and OspC from B. burgdorferi sensu stricto strains share a common evolutionary origin.
TI Evolution of the ***Borrelia*** burgdorferi outer surface protein OspC.
AB The genes coding for outer surface protein OspC from 22 ***Borrelia*** burgdorferi strains isolated from patients with Lyme ***borreliosis*** were cloned and sequenced. For reference purposes, the 16S rRNA genes from 17 of these strains were sequenced after being. . . group contained ospC alleles from all (n = 13) sensu stricto strains, the second group contained ospC alleles from seven ***Borrelia*** afzelii strains, and the third group contained ospC alleles from five B. afzelii and all (n = 9) ***Borrelia*** garinii strains. The ratio of the mean number of synonymous (d-S) and nonsynonymous (d-N) nucleotide substitutions per site calculated for. . . the amino acid level in the relatively variable region. On the basis of the comparison of 16S rRNA gene sequences, ***Borrelia*** hermsii is more closely related to B.

afzelii than to B. burgdorferi sensu stricto and B. garinii. In contrast, the phylogenetic tree obtained for the B. hermsii variable major protein, ***Vmp33*** , and 18 OspC amino acid sequences suggested that ***Vmp33*** and OspC from B. burgdorferi sensu stricto strains share a common evolutionary origin.

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia afzelii
Borrelia burgdorferi
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 62 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 37
AN 1994:345519 BIOSIS <<LOGINID::20090609>>
DN PREV199497358519
TI A family of surface-exposed proteins of 20 kilodaltons in the genus ***Borrelia*** .
AU Carter, Carol J.; Bergstrom, Sven; Norris, Steven J.; Barbour, Alan G. [Reprint author]
CS Dep. Microbiol. and Med., Univ. Texas Health Sci. Cent., San Antonio, TX 78284-7758, USA
SO Infection and Immunity, (1994) Vol. 62, No. 7, pp. 2792-2799.
CODEN: INFIBR. ISSN: 0019-9567.
DT Article
LA English
OS Genbank-L24911
ED Entered STN: 8 Aug 1994
Last Updated on STN: 1 Sep 1994
AB Relapsing fever and Lyme disease spirochetes of the genus ***Borrelia*** display at their surfaces abundant lipoproteins: ***Vmp*** proteins in ***Borrelia*** hermsii and Osp proteins in ***Borrelia*** burgdorferi. ***Vmp*** and Osp proteins largely determine serotype specificity, and neutralizing antibodies of infected or immunized animals are directed at them. For the present study, we examined B. hermsii serotype 33, which is unique among strain HS1 serotypes in the low frequency of switches to other serotypes during infections and in vitro cultivation. Failing to clone the complete ***vmp33*** gene, we accomplished its further characterization by (i) determining three partial amino acid sequences, (ii) designing oligonucleotide primers based on these amino acid sequences, (iii) cloning and sequencing the central portion of ***vmp33*** , and (iv) using outwardly directed primers and the inverse PCR to clone the 5' and 3' ends of the gene and flanking regions. The transcriptional start site was identified by primer extension analysis. ***Vmp33*** was a polypeptide of 211 amino acids; the three partial amino acid sequences were identified in the open reading frame. ***Vmp33*** was found to be more similar to other 20-kDa ***Vmp*** proteins of B. hermsii and to OspC proteins of B. burgdorferi than t was to 35- to 39-kDa ***Vmp*** proteins of the same strain. Moreover, OspC proteins were more similar to ***Vmp33*** than they were to OspA, -B, or -D proteins of B. burgdorferi. These sequence similarities were consistent with Western blot (immunoblot) findings of crossreactions between ***Vmp33*** and OspC with anti- ***Vmp33*** and anti-OspC sera. The promoter for the expressed ***vmp33*** gene

was found to be different from the expression site for other active ***vmp*** genes characterized to date. These results indicate that ***Vmp33*** and other small ***Vmp*** 's belong with OspC to a genus-wide family of 20-kDa proteins and that expression of these proteins may be coordinated with expression of other ***Vmp*** and Osp proteins in ***Borrelia*** spp.

TI A family of surface-exposed proteins of 20 kilodaltons in the genus ***Borrelia*** .

AB Relapsing fever and Lyme disease spirochetes of the genus ***Borrelia*** display at their surfaces abundant lipoproteins: ***Vmp*** proteins in ***Borrelia*** hermsii and Osp proteins in ***Borrelia*** burgdorferi. ***Vmp*** and Osp proteins largely determine serotype specificity, and neutralizing antibodies of infected or immunized animals are directed at them. For. . . in the low frequency of switches to other serotypes during infections and in vitro cultivation. Failing to clone the complete ***vmp33*** gene, we accomplished its further characterization by (i) determining three partial amino acid sequences, (ii) designing oligonucleotide primers based on these amino acid sequences, (iii) cloning and sequencing the central portion of ***vmp33*** , and (iv) using outwardly directed primers and the inverse PCR to clone the 5' and 3' ends of the gene and flanking regions. The transcriptional start site was identified by primer extension analysis. ***Vmp33*** was a polypeptide of 211 amino acids; the three partial amino acid sequences were identified in the open reading frame. ***Vmp33*** was found to be more similar to other 20-kDa ***Vmp*** proteins of B. hermsii and to OspC proteins of B. burgdorferi than t was to 35- to 39-kDa ***Vmp*** proteins of the same strain. Moreover, OspC proteins were more similar to ***Vmp33*** than they were to OspA, -B, or -D proteins of B. burgdorferi. These sequence similarities were consistent with Western blot (immunoblot) findings of crossreactions between ***Vmp33*** and OspC with anti- ***Vmp33*** and anti-OspC sera. The promoter for the expressed ***vmp33*** gene was found to be different from the expression site for other active ***vmp*** genes characterized to date. These results indicate that ***Vmp33*** and other small ***Vmp*** 's belong with OspC to a genus-wide family of 20-kDa proteins and that expression of these proteins may be coordinated with expression of other ***Vmp*** and Osp proteins in ***Borrelia*** spp.

IT . . .
sequence data; nucleotide sequence; L24911: Genbank

IT Miscellaneous Descriptors
CLONING STRATEGY; HOMOLOGY; METHOD; OSPC PROTEIN; PROMOTER ANALYSIS; TRANSCRIPTION START SITE; ***VMP33*** GENE

ORGN Classifier
Spirochaetaceae 06112

Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms

Organism Name
Borrelia burgdorferi
Borrelia hermsii

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 63 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 38

AN 1994:498441 BIOSIS <<LOGINID::20090609>>

DN PREV199497511441

TI Antigen diversity in the bacterium B. hermsii through "somatic' mutations in rearrange ***vmp*** genes.
AU Restrepo, Blanca I.; Barbour, Alan G.
CS Dep. Microbiol., Univ. Texas Health Sci. Cent., San Antonio, TX 78284-7758, USA
SO Cell, (1994) Vol. 78, No. 5, pp. 867-876.
CODEN: CELLB5. ISSN: 0092-8674.
DT Article
LA English
ED Entered STN: 28 Nov 1994
Last Updated on STN: 28 Nov 1994
AB B. hermsii counters host immunity with multiphasic antigenic variation. This is conferred by interplasmidic and intraplasmidic rearrangements of ***vmp*** genes. In several Independent events, activation of a silent ***vmp*** gene through intraplasmidic deletions but not interplasmidic recombinations was followed by the appearance at its 5' end of multiple mutations that were not present in the silent gene. The prevalence of mutant alleles in postswitch populations increased during infections. Differences between the silent and expressed genes were at the same nucleotides at which ***vmp*** pseudogenes differed, suggesting these were templates for postswitch gene conversions. The mechanism of this bacterium to generate diversity, namely, intramolecular deletions followed by mutations in the rearranged gene, mirrors the strategy used by vertebrate hosts to eliminate it.
TI Antigen diversity in the bacterium B. hermsii through "somatic' mutations in rearrange ***vmp*** genes.
AB B. hermsii counters host immunity with multiphasic antigenic variation. This is conferred by interplasmidic and intraplasmidic rearrangements of ***vmp*** genes. In several Independent events, activation of a silent ***vmp*** gene through intraplasmidic deletions but not interplasmidic recombinations was followed by the appearance at its 5' end of multiple mutations. . . in postswitch populations increased during infections. Differences between the silent and expressed genes were at the same nucleotides at which ***vmp*** pseudogenes differed, suggesting these were templates for postswitch gene conversions. The mechanism of this bacterium to generate diversity, namely, intramolecular. . .
IT Miscellaneous Descriptors
BACTERIAL VIRULENCE; HOST IMMUNITY; INTRAMOLECULAR DELETION; POSTSWITCH GENE CONVERSION; PSI- ***VMP26*** PSEUDOGENE; SILENT SITE
ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia hermsii
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 64 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 39
AN 1994:128747 BIOSIS <<LOGINID::20090609>>
DN PREV199497141747
TI Variability of a bacterial surface protein and disease expression in a possible mouse model of systemic lyme ***borreliosis*** .
AU Cadavid, Diego; Thomas, D. Denee; Crawley, Ronald; Barbour, Alan G.

[Reprint author]
CS Dep. Microbiol., Univ. Texas Health Sci. Center, 7703 Floyd Curl Dr., San Antonio, TX 78284-7758, USA
SO Journal of Experimental Medicine, (1994) Vol. 179, No. 2, pp. 631-642.
CODEN: JEMEAV. ISSN: 0022-1007.
DT Article
LA English
ED Entered STN: 24 Mar 1994
Last Updated on STN: 24 Mar 1994
AB During persistent infection of scid mice with ***Borrelia*** turicatae, an agent of relapsing fever and neuroborreliosis, there was variation in the surface proteins the bacteria expressed and in disease manifestations over time. Two serotypes, A and B, were isolated from the mice, cloned by limiting dilution, and further characterized. The only discernible difference between the two variants was in the size of the major surface protein they expressed: serotype A had a variable major protein (***Vmp***) of 23,000, and serotype B had a ***Vmp*** of 20,000. When other scid mice were inoculated with clonal populations of A and B, the infections were similar with respect to onset and degree of spirochetemia, involvement of the eye and heart, and occurrence of a peripheral vestibular disorder. However, there were differences between the serotypes in other respects: (a) serotype B but not A caused reddened and significantly enlarged joints, markedly impaired performance on a walking bar, and severe arthritis by histologic examination; (b) serotype A but not B invaded the central nervous system during early infection; and (c) serotype A penetrated monolayers of human umbilical vein endothelial cells more readily than did serotype B. The combination of arthritis, myocarditis, and neurologic disease resembled human Lyme ***borreliosis*** . The findings indicate that differences in disease expression are determined by variable surface proteins of the bacterium and that scid mouse infections with B. turicatae provide a model for the study of the pathogenesis of Lyme ***borreliosis*** and other persistent spirochetal diseases.
TI Variability of a bacterial surface protein and disease expression in a possible mouse model of systemic lyme ***borreliosis*** .
AB During persistent infection of scid mice with ***Borrelia*** turicatae, an agent of relapsing fever and neuroborreliosis, there was variation in the surface proteins the bacteria expressed and in. . . two variants was in the size of the major surface protein they expressed: serotype A had a variable major protein (***Vmp***) of 23,000, and serotype B had a ***Vmp*** of 20,000. When other scid mice were inoculated with clonal populations of A and B, the infections were similar with. . . vein endothelial cells more readily than did serotype B. The combination of arthritis, myocarditis, and neurologic disease resembled human Lyme ***borreliosis*** . The findings indicate that differences in disease expression are determined by variable surface proteins of the bacterium and that scid mouse infections with B. turicatae provide a model for the study of the pathogenesis of Lyme ***borreliosis*** and other persistent spirochetal diseases.
ORGN . . .
Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Rodents, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia turicatae

Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 65 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 40
AN 1994:435145 BIOSIS <<LOGINID::20090609>>
DN PREV199497448145
TI Activation of a ***vmp*** pseudogene in ***Borrelia*** hermsii: An alternate mechanism of antigenic variation during relapsing fever.
AU Restrepo, B. I.; Carter, C. J.; Barbour, A. G. [Reprint author]
CS Dep. Med., Univ. Tex. Health Sci. Cent., San Antonio, TX 78284-7758, USA
SO Molecular Microbiology, (1994) Vol. 13, No. 2, pp. 287-299.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
ED Entered STN: 11 Oct 1994
Last Updated on STN: 11 Oct 1994
AB The relapsing fever agent, ***Borrelia*** hermsii, undergoes multiphasic antigenic variation to evade its host's immune response. A frequently observed switch is serotype 7 to 26. Unlike silent ***vmp*** genes previously characterized, the transcriptionally silent ***vmp26*** sequence was a pseudogene in lacking a start codon. In serotype 7 the location of the silent ***vmp26*** sequence just downstream of ***vmp7*** on the expression plasmid, as well as on the silent plasmid, was also unique. The demonstration of a predicted circular recombination product in serotype 7 but not serotype 21 populations indicates that the pseudogene was activated by an intramolecular recombination producing a deletion of DNA between 20-nucleotide direct repeats in ***vmp7*** and PSI ***vmp26*** .
TI Activation of a ***vmp*** pseudogene in ***Borrelia*** hermsii: An alternate mechanism of antigenic variation during relapsing fever.
AB The relapsing fever agent, ***Borrelia*** hermsii, undergoes multiphasic antigenic variation to evade its host's immune response. A frequently observed switch is serotype 7 to 26. Unlike silent ***vmp*** genes previously characterized, the transcriptionally silent ***vmp26*** sequence was a pseudogene in lacking a start codon. In serotype 7 the location of the silent ***vmp26*** sequence just downstream of ***vmp7*** on the expression plasmid, as well as on the silent plasmid, was also unique. The demonstration of a predicted circular. . . indicates that the pseudogene was activated by an intramolecular recombination producing a deletion of DNA between 20-nucleotide direct repeats in ***vmp7*** and PSI ***vmp26*** .
ORGN . . .
Notes
Animals, Chordates, Humans, Mammals, Primates, Vertebrates
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia hermsii
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 66 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 41
AN 1994:357938 BIOSIS <<LOGINID::20090609>>

DN PREV199497370938
TI Homology between ***Borrelia*** burgdorferi OspC and members of the family of ***Borrelia*** hermsii variable major proteins.
AU Margolis, Neil; Hogan, Daniel; Cieplak., Witold, Jr.; Schwan, Tom G.; Rosa, Patricia A. [Reprint author]
CS Lab. Microbial Structure and Function, Rocky Mountain Lab., Natl. Inst. Health, Natl. Inst. Allergy and Infectious Dis., Hamilton, MT 59840, USA
SO Gene (Amsterdam), (1994) Vol. 143, No. 1, pp. 105-110.
CODEN: GENED6. ISSN: 0378-1119.
DT Article
LA English
ED Entered STN: 23 Aug 1994
Last Updated on STN: 23 Aug 1994
AB Synthesis of the ***Borrelia*** burgdorferi outer surface protein C (OspC) is quite variable. We have cloned and sequenced the ospC gene from B. burgdorferi isolate CA-11.2A, a clone in which ospC expression varies. The 5' flanking region of the gene contains at least two consensus promoter regions, as well as two large overlapping inverted repeats. Sequence comparison to other OspC proteins indicated that the CA-11.2A OspC is as closely related to OspC from two different genospecies of Lyme disease spirochetes as it is to OspC from the prototype B. burgdorferi strain, B31. Comparisons of the OspC amino acid (aa) sequence with those in aa sequence databases revealed partial identity with the variable major proteins ***Vmp3*** and ***Vmp24*** of B. hermsii, a causative agent of tick-borne relapsing fever. An ospC probe hybridized to B. hermsii restriction fragments and linear plasmids that also were recognized by the ***vmp3*** and ***vmp24*** probes. OspC and these ***Vmp*** appear to be related, but their synthesis is regulated differently in the two species of spirochetes. This represents a fascinating example of the evolution of the number, position, regulation and perhaps function of homologous genes in two related pathogens. These parameters may relate to characteristic properties of the pathogens and their separate tick vectors.
TI Homology between ***Borrelia*** burgdorferi OspC and members of the family of ***Borrelia*** hermsii variable major proteins.
AB Synthesis of the ***Borrelia*** burgdorferi outer surface protein C (OspC) is quite variable. We have cloned and sequenced the ospC gene from B. burgdorferi. . . the OspC amino acid (aa) sequence with those in aa sequence databases revealed partial identity with the variable major proteins ***Vmp3*** and ***Vmp24*** of B. hermsii, a causative agent of tick-borne relapsing fever. An ospC probe hybridized to B. hermsii restriction fragments and linear plasmids that also were recognized by the ***vmp3*** and ***vmp24*** probes. OspC and these ***Vmp*** appear to be related, but their synthesis is regulated differently in the two species of spirochetes. This represents a fascinating. . .
ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia burgdorferi
Borrelia hermsii
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 67 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on

STN DUPLICATE 42

AN 1993:299705 BIOSIS <<LOGINID::20090609>>

DN PREV199396017930

TI Intragenic recombination and a chimeric outer membrane protein in the relapsing fever agent ***Borrelia*** hermsii.

AU Kitten, Todd; Barrera, Adrian V.; Barbour, Alan G. [Reprint author]

CS Dep. Microbiol. Med., Univ. Texas Health Sci. Center, San Antonio, Texas 78284-7758, USA

SO Journal of Bacteriology, (1993) Vol. 175, No. 9, pp. 2516-2522. CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 23 Jun 1993
Last Updated on STN: 23 Jun 1993

AB The spirochete ***Borrelia*** hermsii, a relapsing fever agent, evades the host's immune response through multiphasic antigenic variation. Antigen switching results from sequential expression of genes for serotype-specific outer membrane proteins known as variable major proteins (***Vmp*** 's); of the 25 serotypes that have been identified for the HS1 strain, serotypes 7 and 21 have been studied in greatest detail. In the present study, an atypical variant was predominant in the relapse from a serotype 21 infection in mice; relapse cells were bound by monoclonal antibodies specific for ***Vmp21*** as well as antibodies specific for ***Vmp7*** . In Western blots (immunoblots), the variant had a single ***Vmp*** that was reactive with monoclonal antibodies representing both serotypes. The gene encoding this ***Vmp*** , ***vmp7*** /21, was cloned and characterized by restriction mapping and sequence analysis to determine the likely recombination event. Whereas the 5' end of ***vmp7*** /21 was identical to that of ***vmp21*** , its 3' end and flanking sequences were identical to the 3' end of ***vmp7*** . Unlike other ***vmp*** genes examined thus far, the ***vmp7*** /21 gene existed only in an expressed form; a silent, storage form of the gene was not detected. We conclude that the ***vmp7*** /21 gene was created by an intragenic recombination between the formerly expressed ***vmp21*** gene and a silent ***vmp7*** gene. This finding suggests that the lack of cross-reactivity between variants, which is usually observed, results from immunoselection against variants possessing chimeric ***Vmp*** 's rather than from a switching mechanism that excludes partial gene replacements.

TI Intragenic recombination and a chimeric outer membrane protein in the relapsing fever agent ***Borrelia*** hermsii.

AB The spirochete ***Borrelia*** hermsii, a relapsing fever agent, evades the host's immune response through multiphasic antigenic variation. Antigen switching results from sequential expression of genes for serotype-specific outer membrane proteins known as variable major proteins (***Vmp*** 's); of the 25 serotypes that have been identified for the HS1 strain, serotypes 7 and 21 have been studied in. . . predominant in the relapse from a serotype 21 infection in mice; relapse cells were bound by monoclonal antibodies specific for ***Vmp21*** as well as antibodies specific for ***Vmp7*** . In Western blots (immunoblots), the variant had a single ***Vmp*** that was reactive with monoclonal antibodies representing both serotypes. The gene encoding this ***Vmp*** , ***vmp7*** /21, was cloned and characterized by restriction mapping and sequence analysis to determine the likely recombination event. Whereas the 5' end of ***vmp7*** /21 was

identical to that of ***vmp21*** , its 3' end and flanking sequences were identical to the 3' end of ***vmp7*** . Unlike other ***vmp*** genes examined thus far, the ***vmp7*** /21 gene existed only in an expressed form; a silent, storage form of the gene was not detected. We conclude that the ***vmp7*** /21 gene was created by an intragenic recombination between the formerly expressed ***vmp21*** gene and a silent ***vmp7*** gene. This finding suggests that the lack of cross-reactivity between variants, which is usually observed, results from immunoselection against variants possessing chimeric ***Vmp*** 's rather than from a switching mechanism that excludes partial gene replacements.

IT Miscellaneous Descriptors
ANTIGEN SWITCHING MECHANISM; GENE MAPPING; IMMUNE SELECTION; RESTRICTION MAPPING; ***VMP21*** GENE; ***VMP7*** GENE; ***VMP7*** -21 GENE

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia hermsii
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 68 OF 87 MEDLINE on STN
AN 1994184809 MEDLINE <<LOGINID::20090609>>
DN PubMed ID: 8137122
TI Linear DNA of ***Borrelia*** species and antigenic variation.
AU Barbour A G
CS Dept of Microbiology, University of Texas Health Science Center, San Antonio 78284.
NC AI24424 (United States NIAID NIH HHS)
AI29731 (United States NIAID NIH HHS)
AR41507 (United States NIAMS NIH HHS)
+
SO Trends in microbiology, (1993 Sep) Vol. 1, No. 6, pp. 236-9.
Journal code: 9310916. ISSN: 0966-842X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Priority Journals
EM 199404
ED Entered STN: 9 May 1994
Last Updated on STN: 9 May 1994
Entered Medline: 28 Apr 1994
AB Members of the genus ***Borrelia*** may be unique among prokaryotic organisms in having a polyploid genome that is mostly linear. The smaller linear duplex replicons in these organisms have been called plasmids, but there is justification for designating them minichromosomes instead. The antigenic identities of the agents of Lyme disease and relapsing fever are largely determined by these extrachromosomal genes.
TI Linear DNA of ***Borrelia*** species and antigenic variation.
AB Members of the genus ***Borrelia*** may be unique among prokaryotic organisms in having a polyploid genome that is mostly linear. The smaller linear duplex replicons. . .

CT *Antigenic Variation: GE, genetics
Bacterial Outer Membrane Proteins: GE, genetics
Base Sequence
****Borrelia: GE, genetics***
*** Borrelia: IM, immunology***
*DNA, Bacterial: GE, genetics
Genome, Bacterial
Molecular Sequence Data
Plasmids: GE, genetics
GEN osp; ***vmp***

L4 ANSWER 69 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN DUPLICATE 43
AN 1994:74507 CAPLUS <<LOGINID::20090609>>
DN 120:74507
OREF 120:13359a,13362a
TI Experimental infection of the mouse brain by a relapsing fever ***Borrelia*** species: a molecular analysis
AU Cadavid, Diego; Bundoc, Virgilio; Barbour, Alan G.
CS Health Sci. Cent., Univ. Texas, San Antonio, TX, 78284-7758, USA
SO Journal of Infectious Diseases (1993), 168(1), 143-51
CODEN: JIDIAQ; ISSN: 0022-1899
DT Journal
LA English
AB The spirochetal disease relapsing fever is notable not only for multiphasic antigenic variation but also for central neurol. manifestations. To further characterize involvement of the brain in this disorder, immunocompetent and immunodeficient mice were infected with ***Borrelia*** hermsii. Immunodeficient mice were treated while spirochetemic with neutralizing IgM monoclonal antibodies to the infecting serotype. Blood, cerebrospinal fluid, and brain tissue were examd. by culture and polymerase chain reaction. In immunocompetent mice, antigenic variation occurred in the brain as well as in the blood. In immunodeficient mice, the infecting serotype was still present in the brain after it had been eliminated from the blood by the administered antibodies. These latter results cannot be accounted for by contamination of brain tissue and cerebrospinal fluid by blood and, hence, establish the direct involvement of the central nervous system in this exptl. infection.
TI Experimental infection of the mouse brain by a relapsing fever ***Borrelia*** species: a molecular analysis
AB . . . central neurol. manifestations. To further characterize involvement of the brain in this disorder, immunocompetent and immunodeficient mice were infected with ***Borrelia*** hermsii. Immunodeficient mice were treated while spirochetemic with neutralizing IgM monoclonal antibodies to the infecting serotype. Blood, cerebrospinal fluid, and. . .
ST ***Borrelia*** brain antigen ***Vmp*** protein sequence; gene ***vmp*** ***Borrelia*** brain sequence
IT Antigens
RL: BIOL (Biological study)
(***Borrelia*** hermsii variable major protein New ***Vmp*** as, in relapsing fever)
IT Gene, microbial
RL: BIOL (Biological study)
(new ***vmp*** , nucleotide sequence of, of ***Borrelia*** hermsii, relapsing fever in relation to)
IT Deoxyribonucleic acid sequences
(of gene new ***vmp*** of ***Borrelia*** hermsii, relapsing

fever in relation to)
IT Protein sequences
(of variable major protein New ***Vmp*** of ***Borrelia*** hermsii, relapsing fever in relation to)
IT ***Borrelia*** hermsii
(variable major protein New ***Vmp*** of, amino acid sequence of, relapsing fever in relation to)
IT Brain, disease
(infection, with ***Borrelia*** hermsii, variable major protein New ***Vmp*** in)
IT Fever and Hyperthermia
(relapsing, from ***Borrelia*** hermsii infection of brain, variable major protein New ***Vmp*** in)
IT 152522-18-4, Protein (***Borrelia*** hermsii clone bp7E variable major protein New ***Vmp***)
RL: PRP (Properties)
(amino acid sequence of)
IT 152522-17-3, DNA (***Borrelia*** hermsii clone bp7E gene new ***vmp*** mRNA-complementary)
RL: PRP (Properties)
(nucleotide sequence of)

L4 ANSWER 70 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 44
AN 1993:94463 BIOSIS <<LOGINID::20090609>>
DN PREV199395049659
TI Subtelomeric expression regions of ***Borrelia*** hermsii linear plasmids are highly polymorphic.
AU Restrepo, B. I.; Kitten, T.; Carter, C. J.; Infante, D.; Barbour, A. G. [Reprint author]
CS Dep. Microbiol., Univ. Tex. Health Sci. Cent., San Antonio, Tex. 78284-7758, USA
SO Molecular Microbiology, (1992) Vol. 6, No. 22, pp. 3299-3311.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
LA English
OS DDBJ-LO4786; DDBJ-LO4787; DDBJ-LO4788; DDBJ-LO4789; DDBJ-MS7256; DDBJ-Z11876; EMBL-LO4786; EMBL-LO4787; EMBL-LO4788; EMBL-LO4789; EMBL-MS7256; EMBL-Z11876; Genbank-LO4786; Genbank-LO4787; Genbank-LO4788; Genbank-LO4789; Genbank-MS7256; Genbank-Z11876
ED Entered STN: 9 Feb 1993
Last Updated on STN: 17 Apr 1993
AB ***Borrelia*** hermsii, a relapsing fever agent, undergoes multiphasic antigenic variation to evade its host's immune response. Serotype specificity is determined by variable membrane lipoproteins, ***Vmps*** , which are expressed from genes located near the end of a linear plasmid. Using the polymerase chain reaction and primers representing the promoter of the active ***vmp*** and a conserved telomeric sequence, we characterized the subtelomeric expression regions of the 25 known serotypes of strain HS1. The distance from the promoter to the telomere fell into three size classes of approximately 1.0, 1.5, and 2.5 kilobases. In the sequenced serotypes the size differences were accounted for by variable lengths of the ***vmp*** genes and intervening sequences between 3' end of the ***vmp*** gene and the start of a downstream homology block. The degree of nucleotide identify between different ***vmp*** genes, or between the different 3' flanking DNA varied from 39-78%. Thus, there is length and sequence variability not only between

vmp genes themselves but also between the 3' flanking regions of ***vmp*** genes.

TI Subtelomeric expression regions of ***Borrelia*** hermsii linear plasmids are highly polymorphic.

AB ***Borrelia*** hermsii, a relapsing fever agent, undergoes multiphasic antigenic variation to evade its host's immune response. Serotype specificity is determined by variable membrane lipoproteins, ***Vmps*** , which are expressed from genes located near the end of a linear plasmid. Using the polymerase chain reaction and primers representing the promoter of the active ***vmp*** and a conserved telomeric sequence, we characterized the subtelomeric expression regions of the 25 known serotypes of strain HS1. The. . . 1.0, 1.5, and 2.5 kilobases. In the sequenced serotypes the size differences were accounted for by variable lengths of the ***vmp*** genes and intervening sequences between 3' end of the ***vmp*** gene and the start of a downstream homology block. The degree of nucleotide identify between different ***vmp*** genes, or between the different 3' flanking DNA varied from 39-78%. Thus, there is length and sequence variability not only between ***vmp*** genes themselves but also between the 3' flanking regions of ***vmp*** genes.

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia hermsii
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 71 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 45

AN 1993:3952 BIOSIS <<LOGINID::20090609>>

DN PREV199395003952

TI The relapsing fever agent ***Borrelia*** hermsii has multiple copies of its chromosome and linear plasmids.

AU Kitten, Todd [Reprint author]; Barbour, Alan G.

CS Dep. Microbiol., University Texas Health Sci. Center, San Antonio, Texas 78284, USA

SO Genetics, (1992) Vol. 132, No. 2, pp. 311-324.
CODEN: GENTAE. ISSN: 0016-6731.

DT Article

LA English

ED Entered STN: 10 Dec 1992
Last Updated on STN: 10 Dec 1992

AB ***Borrelia*** hermsii, a spirochete which causes relapsing fever in humans and other mammals, eludes the immune response by antigenic variation of the " ***Vmp*** " proteins. This occurs by replacement of an expressed ***vmp*** gene with a copy of a silent ***vmp*** gene. Silent and expressed ***vmp*** genes are located on separate linear plasmids. To further characterize ***vmp*** recombination, copy numbers were determined for two linear plasmids and for the 1-megabase chromosome by comparing hybridization of probes to native DNA with hybridization to recombinant plasmids containing ***borrelial*** DNA. Plasmid copy numbers were also estimated by ethidium bromide fluorescence. Total cellular DNA content was determined by spectrophotometry. For ***borrelias*** grown in mice, copy numbers and 95% confidence intervals were 14 (12-17) for an expression plasmid, 8

(7-9) for a silent plasmid, and 16 (13-18) for the chromosome.
Borrelias grown in broth medium had one-fourth to one-half this number of plasmids and chromosomes. Staining of cells with 4',6-diamidino-2-phenylindole revealed DNA to be distributed throughout most of the spirochete's length. These findings indicate that
borrelias organize their total cellular DNA into several complete genomes and that cells undergoing serotype switches do one or more of the following: (1) coexpress ***Vmps*** from switched and unswitched expression plasmids for at least three to five generations, (2) suppress transcription from some expression plasmid copies, or (3) partition expression plasmids nonrandomly. The lower copy number of the silent plasmid indicates that nonreciprocal ***Vmp*** gene recombination may result from loss of recombinant silent plasmids by segregation.

TI The relapsing fever agent ***Borrelia*** hermsii has multiple copies of its chromosome and linear plasmids.

AB ***Borrelia*** hermsii, a spirochete which causes relapsing fever in humans and other mammals, eludes the immune response by antigenic variation of the " ***Vmp*** " proteins. This occurs by replacement of an expressed ***vmp*** gene with a copy of a silent ***vmp*** gene. Silent and expressed ***vmp*** genes are located on separate linear plasmids. To further characterize ***vmp*** recombination, copy numbers were determined for two linear plasmids and for the 1-megabase chromosome by comparing hybridization of probes to native DNA with hybridization to recombinant plasmids containing ***borrelial*** DNA. Plasmid copy numbers were also estimated by ethidium bromide fluorescence. Total cellular DNA content was determined by spectrophotometry. For ***borrelias*** grown in mice, copy numbers and 95% confidence intervals were 14 (12-17) for an expression plasmid, 8 (7-9) for a silent plasmid, and 16 (13-18) for the chromosome.
Borrelias grown in broth medium had one-fourth to one-half this number of plasmids and chromosomes. Staining of cells with 4',6-diamidino-2-phenylindole revealed DNA to be distributed throughout most of the spirochete's length. These findings indicate that
borrelias organize their total cellular DNA into several complete genomes and that cells undergoing serotype switches do one or more of the following: (1) coexpress ***Vmps*** from switched and unswitched expression plasmids for at least three to five generations, (2) suppress transcription from some expression plasmid copies, or (3) partition expression plasmids nonrandomly. The lower copy number of the silent plasmid indicates that nonreciprocal ***Vmp*** gene recombination may result from loss of recombinant silent plasmids by segregation.

IT Miscellaneous Descriptors
ANTIGENIC VARIATION; ***VMP*** GENE EXPRESSION; ***VMP*** PROTEIN

ORGN Classifier
Spirochaetaceae 06112
Super Taxa
Spirochaetales; Spirochetes; Eubacteria; Bacteria; Microorganisms
Organism Name
Borrelia hermsii
Taxa Notes
Bacteria, Eubacteria, Microorganisms

L4 ANSWER 72 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 46

AN 1991:510076 BIOSIS <<LOGINID::20090609>>

DN PREV199141110791; BR41:110791

TI ANTIGENIC VARIATION IN ***BORRELIA*** .
AU GIRONS I S [Reprint author]; BARBOUR A G
CS UNITE LEPTOSPIRES, INST PASTEUR, 75724 PARIS CEDEX 15
SO Research in Microbiology, (1991) Vol. 142, No. 6, pp. 711-718.
CODEN: RMCREW. ISSN: 0923-2508.
DT Article
FS BR
LA ENGLISH
ED Entered STN: 14 Nov 1991
Last Updated on STN: 14 Nov 1991
TI ANTIGENIC VARIATION IN ***BORRELIA*** .
IT Miscellaneous Descriptors
REVIEW ***BORRELIA*** -HERMSII RELAPSING FEVER MAJOR SURFACE PROTEIN ***VMP*** GENES PLASMID GENE TRANSPOSITION GENE ACTIVATION TELOMERIC SITE REARRANGEMENT

L4 ANSWER 73 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 47
AN 1991:226831 BIOSIS <<LOGINID::20090609>>
DN PREV199191118291; BA91:118291
TI VARIABLE ANTIGEN GENES OF THE RELAPSING FEVER AGENT ***BORRELIA*** -HERMSII ARE ACTIVATED BY PROMOTER ADDITION.
AU BARBOUR A G [Reprint author]; BURMAN N; CARTER C J; KITTEN T; BERGSTROM S
CS DEP MICROBIOL AND MED, UNIV TEX HEALTH SCI CENT, SAN ANTONIO, TEX 78284, USA
SO Molecular Microbiology, (1991) Vol. 5, No. 2, pp. 489-494.
CODEN: MOMIEE. ISSN: 0950-382X.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 9 May 1991
Last Updated on STN: 9 May 1991
AB ***Borrelia*** hermsii, an agent of relapsing fever, avoids the host's immune response by means of multiphasia antigenic variation. Serotype specificity is determined by variable antigens called the ***Vmp*** lipoproteins. Through recombination between linear plasmids a formerly silent ***vmp*** gene replaces another ***vmp*** gene at a telomeric expression locus. We examined strain HS1 ***borreliae*** before and after a switch from serotype 7 to serotype 21. The nucleotide sequences of 5' regions of silent and expressed ***vmp7*** and ***vmp21*** were determined. Silent and active ***vmp7*** and ***vmp21*** genes shared a block of homologous sequences surrounding their 5' ends. Sequences upstream of silent ***vmp7*** and ***vmp21*** genes lacked the promoter and substantially differed from each other. In this antigenic switch a ***vmp*** gene was activated by a recombination that placed it downstream of a promoter.
TI VARIABLE ANTIGEN GENES OF THE RELAPSING FEVER AGENT ***BORRELIA*** -HERMSII ARE ACTIVATED BY PROMOTER ADDITION.
AB ***Borrelia*** hermsii, an agent of relapsing fever, avoids the host's immune response by means of multiphasia antigenic variation. Serotype specificity is determined by variable antigens called the ***Vmp*** lipoproteins. Through recombination between linear plasmids a formerly silent ***vmp*** gene replaces another ***vmp*** gene at a telomeric expression locus. We examined strain HS1 ***borreliae*** before and after a switch from serotype 7 to serotype 21. The nucleotide sequences of 5' regions of silent and expressed ***vmp7*** and ***vmp21*** were determined. Silent and active ***vmp7*** and

vmp21 genes shared a block of homologous sequences surrounding their 5' ends. Sequences upstream of silent ***vmp7*** and ***vmp21*** genes lacked the promoter and substantially differed from each other. In this antigenic switch a ***vmp*** gene was activated by a recombination that placed it downstream of a promoter.

IT Miscellaneous Descriptors
LIPOPROTEIN ***VMP*** GENE RECOMBINATION NUCLEOTIDE SEQUENCE MOLECULAR SEQUENCE DATA

L4 ANSWER 74 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 48

AN 1991:113384 BIOSIS <<LOGINID::20090609>>

DN PREV199191060774; BA91:60774

TI TANDEM INSERTION SEQUENCE-LIKE ELEMENTS DEFINE THE EXPRESSION SITE FOR VARIABLE ANTIGEN GENES OF ***BORRELIA*** -HERMSII.

AU BARBOUR A G [Reprint author]; CARTER C J; BURMAN N; FREITAG C S; GARON C F; BERGSTROM S

CS DEP MICROBIOL, UNIV TEXAS HEALTH SCI CENT, SAN ANTONIO, TX 78284, USA

SO Infection and Immunity, (1991) Vol. 59, No. 1, pp. 390-397.
CODEN: INFIBR. ISSN: 0019-9567.

DT Article

FS BA

LA ENGLISH

ED Entered STN: 27 Feb 1991
Last Updated on STN: 27 Feb 1991

AB The spirochete ***Borrelia*** hermsii avoids the immune response of its mammalian host through multiphasic antigenic variation. Serotype specificity is determined by variable antigens, ***Vmp*** proteins, in the outer membrane. Through nonreciprocal recombination between linear plasmids, a formerly silent ***vmp*** gene replaces another ***vmp*** gene downstream from a common expression site. To futher characterize this activating site, we determined the nucleotide sequence of 6.9 kb of the common upstream expression region of strain HS1 of B. hermsii. Preceding the ***vmp*** gene promoter and a poly(dT .cntdot. dA) run were three imperfectly repeated segments of 2 kb. Each of the 2-kb segments contained 1-kb elements with inverted repeats of approximately 0.2 kb each at their termini. The potential of the 1-kb elements to form stem-and-loop structures was demonstrated by heteroduplex analysis. There was no evidence of the presence of the elements elsewhere in the genome of B. hermsii. One or more of these elements may confer the unidirectionality that characterizes ***vmp*** gene switches.

TI TANDEM INSERTION SEQUENCE-LIKE ELEMENTS DEFINE THE EXPRESSION SITE FOR VARIABLE ANTIGEN GENES OF ***BORRELIA*** -HERMSII.

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L4 ANSWER 75 OF 87 CABA COPYRIGHT 2009 CABI on STN
AN 91:89224 CABA <<LOGINID::20090609>>
DN 19910506221
TI Antigenic variation in relapsing fever ***Borrelia*** species
AU Barbour, A. G.; Iglewski, B.H. [EDITOR]; Clark, V.L. [EDITOR]
CS Departments of Microbiology and Medicine, University of Texas Health Science Center, San Antonio, TX 78284, USA.
SO The bacteria: a treatise on structure and function. Volume XI. Molecular basis of bacterial pathogenesis, (1990) pp. 155-176. 44 ref. Publisher: Academic Press, Inc. San Diego, California
CY United States
DT Miscellaneous
LA English
ED Entered STN: 1 Nov 1994
Last Updated on STN: 1 Nov 1994
AB Antigenic variation in relapsing fever species of ***Borrelia*** , including B. hermsii, B. duttonii and B. turicatae, is reviewed. Subjects discussed include virulence properties, clinical and experimental infections, variable antigens, active and silent genes for variable antigens, linear plasmids, and models for the mechanism of ***vmp*** switching.
TI Antigenic variation in relapsing fever ***Borrelia*** species.
AB Antigenic variation in relapsing fever species of ***Borrelia*** , including B. hermsii, B. duttonii and B. turicatae, is reviewed. Subjects discussed include virulence properties, clinical and experimental infections, variable antigens, active and silent genes for variable antigens, linear plasmids, and models for the mechanism of ***vmp*** switching.
BT Spirochaetales; Gracilicutes; bacteria; prokaryotes; ***Borrelia*** ; Spirochaetaceae
ORGN Spirochaetaceae; ***Borrelia*** hermsii; ***Borrelia*** duttonii; ***Borrelia*** turicatae

L4 ANSWER 76 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1991:104960 BIOSIS <<LOGINID::20090609>>
DN PREV199140047780; BR40:47780
TI MULTIPHASIC ANTIGENIC VARIATION IN THE BACTERIUM THAT CAUSES RELAPSING FEVER.
AU BARBOUR A G [Reprint author]
CS DEP MICROBIOL, UNIV TEXAS HEALTH SCI CENT, SAN ANTONIO, TEXAS 78284, USA
SO (1990) pp. 183-200. VAN DER PLOEG, L. H. T., C. R. CANTOR AND H. J. VOGEL (ED.). IMMUNE RECOGNITION AND EVASION: MOLECULAR ASPECTS OF HOST-PARASITE INTERACTION; P AND S BIOMEDICAL SCIENCES SYMPOSIUM, NEW YORK, NEW YORK, USA, JUNE 3-5, 1988. XIII+315P. ACADEMIC PRESS, INC.: SAN DIEGO, CALIFORNIA, USA; LONDON, ENGLAND, UK. ILLUS.
ISBN: 0-12-711710-5.
DT Book
Conference; (Meeting)
FS BR
LA ENGLISH
ED Entered STN: 26 Feb 1991
Last Updated on STN: 26 Feb 1991
IT Miscellaneous Descriptors
BORRELIA HUMAN RAT ***VMP*** GENE OUTER MEMBRANE PROTEIN

L4 ANSWER 77 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on

STN
AN 1991:15290 BIOSIS <<LOGINID::20090609>>
DN PREV199140003620; BR40:3620
TI ANTIGENIC VARIATION OF A RELAPSING FEVER ***BORRELIA*** SPECIES.
AU BARBOUR A G [Reprint author]
CS DEP MICROBIOL MEDICINE, UNIVERSITY TEXAS HEALTH SCIENCE CENTER SAN ANTONIO, SAN ANTONIO, TEXAS 78284, USA
SO Annu. Rev. Microbiol., (1990) pp. 155-172. ORNSTON, N. L. (ED.). ANNUAL REVIEW OF MICROBIOLOGY, VOL. 44. XIII+748P. ANNUAL REVIEWS INC.: PALO ALTO, CALIFORNIA, USA. ILLUS.
Publisher: Series: Annual Review of Microbiology.
CODEN: ARMIAZ. ISSN: 0066-4227. ISBN: 0-8243-1144-2.
DT Book
FS BR
LA ENGLISH
ED Entered STN: 11 Dec 1990
Last Updated on STN: 11 Dec 1990
TI ANTIGENIC VARIATION OF A RELAPSING FEVER ***BORRELIA*** SPECIES.
IT Miscellaneous Descriptors
REVIEW OUTER MEMBRANE PROTEIN DNA REARRANGEMENT PLASMID ***VMP*** GENES

L4 ANSWER 78 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 49
AN 1990:448185 BIOSIS <<LOGINID::20090609>>
DN PREV199090098825; BA90:98825
TI JUXTAPOSITION OF EXPRESSED VARIABLE ANTIGEN GENES WITH A CONSERVED TELOMERE IN THE BACTERIUM ***BORRELIA*** -HERMSII.
AU KITTEN T [Reprint author]; BARBOUR A G
CS DEP MICROBIOLOGY, UNIVERSITY TEXAS HEALTH SCI CENTER, SAN ANTONIO, TEXAS 78284, USA
SO Proceedings of the National Academy of Sciences of the United States of America, (1990) Vol. 87, No. 16, pp. 6077-6081.
CODEN: PNASA6. ISSN: 0027-8424.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 7 Oct 1990
Last Updated on STN: 7 Oct 1990
AB ***Borrelia*** hermsii, an agent of relapsing fever, survives in mammals through antigenic variation. Change in serotype-specific variable outer membrane proteins (***Vmps***) occurs when a ***Vmp*** gene at an expression site is replaced with a previously silent gene for another ***Vmp*** . Silent and active genes are on separate linear plasmids. The upstream site for a nonreciprocal recombination between two linear plasmids is near the 5' ends of the expressed and silent genes. In the present study we sought the downstream recombination sites in two serotypes, 7 and 21. Restriction fragments containing plasmid telomeres were identified by susceptibility to digestion with BAL-31 and rapid reannealment following denaturation. Whereas both silent genes and a minority population of both expression-linked genes were several kilobases from the telomeres, the predominant population of both expressed genes had 3' ends near plasmid telomeres. Sequence analysis of the predominant expression plasmids revealed that the telomeric sequences were the same in serotypes 7 and 21. Identical sequence was also downstream of silent ***Vmp*** genes. Switching of ***Vmp*** genes appears to occur by recombination that involves both upstream and downstream sites. The

expression plasmid's telomere is preserved in the recombination event.

TI JUXTAPOSITION OF EXPRESSED VARIABLE ANTIGEN GENES WITH A CONSERVED TELOMERE IN THE BACTERIUM ***BORRELIA*** -HERMSII.

AB ***Borrelia*** hermsii, an agent of relapsing fever, survives in mammals through antigenic variation. Change in serotype-specific variable outer membrane proteins (***Vmps***) occurs when a ***Vmp*** gene at an expression site is replaced with a previously silent gene for another ***Vmp*** . Silent and active genes are on separate linear plasmids. The upstream site for a nonreciprocal recombination between two linear plasmids. . . revealed that the telomeric sequences were the same in serotypes 7 and 21. Identical sequence was also downstream of silent ***Vmp*** genes. Switching of ***Vmp*** genes appears to occur by recombination that involves both upstream and downstream sites. The expression plasmid's telomere is preserved in. . .

L4 ANSWER 79 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 50

AN 1991:31053 BIOSIS <<LOGINID::20090609>>

DN PREV199191020404; BA91:20404

TI THE VARIABLE ANTIGENS ***VMP7*** AND ***VMP21*** OF THE RELAPSING FEVER BACTERIUM ***BORRELIA*** -HERMSII ARE STRUCTURALLY ANALOGOUS TO THE VSG PROTEINS OF THE AFRICAN TRYPANOSOME.

AU BURMAN N [Reprint author]; BERGSTROM S; RESTREPO B I; BARBOUR A G

CS DEP MICROBIOL, UNIV UMEA, S-901 87 UMEA, SWEDEN

SO Molecular Microbiology, (1990) Vol. 4, No. 10, pp. 1715-1726. CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

FS BA

LA ENGLISH

OS GENBANK-X53926; GENBANK-X53927

ED Entered STN: 3 Jan 1991
Last Updated on STN: 3 Jan 1991

AB The relapsing fever agent ***Borrelia*** hermsii avoids the host's immune response by the strategy of multiphasic antigenic variation. A given ***Borrelia*** cell can express one of a number of alleles for polymorphic outer-membrane proteins, known as ***Vmp*** proteins. The genes for the variant-specific ***Vmp*** proteins of serotypes 7 and 21 of B. hermsii strain HS1 were sequenced. The genes, which were designated ***vmp7*** and ***vmp21*** , were obtained from populations of ***borreliae*** before and after a switch in serotypes from 7 to 21. The analysis showed that ***vmp7*** and ***vmp21*** are 77% identical in terms of their coding sequence. The deduced translation products of ***vmp7*** and ***vmp21*** are polypeptides of 369 (37.2kD) and 364 amino acids (37.1kD), respectively. ***Vmp7*** and ***Vmp21*** have sequence features of prokaryotic lipoproteins and are processed as such during expression in E. coli. The secondary structure predictions of the ***Vmp*** proteins reveals analogous structures to the VSG proteins of the African trypanosome.

TI THE VARIABLE ANTIGENS ***VMP7*** AND ***VMP21*** OF THE RELAPSING FEVER BACTERIUM ***BORRELIA*** -HERMSII ARE STRUCTURALLY ANALOGOUS TO THE VSG PROTEINS OF THE AFRICAN TRYPANOSOME.

AB The relapsing fever agent ***Borrelia*** hermsii avoids the host's immune response by the strategy of multiphasic antigenic variation. A given ***Borrelia*** cell can express one of a number of alleles for polymorphic outer-membrane proteins, known as ***Vmp*** proteins. The genes for the variant-specific ***Vmp*** proteins of serotypes 7 and 21 of B. hermsii strain HS1 were sequenced. The genes, which were

designated ***vmp7*** and ***vmp21*** , were obtained from populations of ***borreliae*** before and after a switch in serotypes from 7 to 21. The analysis showed that ***vmp7*** and ***vmp21*** are 77% identical in terms of their coding sequence. The deduced translation products of ***vmp7*** and ***vmp21*** are polypeptides of 369 (37.2kD) and 364 amino acids (37.1kD), respectively. ***Vmp7*** and ***Vmp21*** have sequence features of prokaryotic lipoproteins and are processed as such during expression in E. coli. The secondary structure predictions of the ***Vmp*** proteins reveals analogous structures to the VSG proteins of the African trypanosome.

L4 ANSWER 80 OF 87 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1991:605225 CAPLUS <<LOGINID::20090609>>
DN 115:205225
OREF 115:35001a,35004a
TI Multiphasic antigenic variation in the bacterium that causes relapsing fever
AU Barbour, Alan G.
CS Health Sci. Cent., Univ. Texas, San Antonio, TX, 78284, USA
SO Immune Recognit. Evasion: Mol. Aspects Host-Parasite Interact. (1990), 183-99. Editor(s): Van der Ploeg, Lex H. T.; Cantor, Charles R.; Vogel, Henry J. Publisher: Academic, San Diego, Calif.
CODEN: 57AEAO
DT Conference; General Review
LA English
AB A review with 27 refs. of multiphasic antigenic variation in ***Borrelia*** and the role of recombination in ***vmp*** (variable major protein) gene switching.
AB A review with 27 refs. of multiphasic antigenic variation in ***Borrelia*** and the role of recombination in ***vmp*** (variable major protein) gene switching.
ST review antigen variation ***Borrelia*** ; gene switching antigen ***Borrelia*** review
IT ***Borrelia***
(antigenic variation in)
IT Gene and Genetic element, microbial
RL: BIOL (Biological study)
(for variable antigens, switching of, in antigenic variation in ***Borrelia***)
IT Recombination, genetic
(in antigenic variation, in ***Borrelia***)
IT Antigens
RL: BIOL (Biological study)
(variability of, in ***Borrelia***)

L4 ANSWER 81 OF 87 CABA COPYRIGHT 2009 CABI on STN DUPLICATE 51
AN 92:127372 CABA <<LOGINID::20090609>>
DN 19920512260
TI Antigenic variation of a relapsing fever ***Borrelia*** species
AU Barbour, A. G.
CS Department of Microbiology and Medicine, University of Texas Health Science Center at San Antonio, San Antonio, TX 78284, USA.
SO Annual Review of Microbiology, (1990) Vol. 44, pp. 155-171. 39 ref.
Publisher: Annual Reviews Inc. Palo Alto, California
ISSN: 0066-4227; ISBN: 0-8243-1144-2
CY United States
DT Journal

LA English
ED Entered STN: 1 Nov 1994
Last Updated on STN: 1 Nov 1994
AB This review examines the immunology of relapsing fever and antigenic variation in B. hermsii. The variable antigens of this spirochaete are outer membrane proteins, and antigenic variation is the consequence of DNA rearrangements. The ***vmp*** genes (of Variable Major Proteins) are located on linear plasmids. The activation of a new ***vmp*** is the result of recombination between different linear plasmids.
TI Antigenic variation of a relapsing fever ***Borrelia*** species.
AB . . . The variable antigens of this spirochaete are outer membrane proteins, and antigenic variation is the consequence of DNA rearrangements. The ***vmp*** genes (of Variable Major Proteins) are located on linear plasmids. The activation of a new ***vmp*** is the result of recombination between different linear plasmids.
BT Spirochaetales; Gracilicutes; bacteria; prokaryotes; ***Borrelia*** ; Spirochaetaceae
ORGN Spirochaetaceae; ***Borrelia*** hermsii

L4 ANSWER 82 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1989:299884 BIOSIS <<LOGINID::20090609>>
DN PREV198937014261; BR37:14261
TI ANTIGENIC VARIATION IN RELAPSING FEVER ***BORRELIA*** SPECIES GENETICS ASPECTS.
AU BARBOUR A [Reprint author]
CS DEP OF MICROBIOL, UNIV OF TEX HEALTH SCI CENT, 7703 FLOYD CURL DRIVE, SAN ANTONIO, TEX 78284-7758, USA
SO (1989) pp. 783-790. BERG, D. E. AND M. M. HOWE (ED.). MOBILE DNA. XVII+972P. AMERICAN SOCIETY FOR MICROBIOLOGY: WASHINGTON, D.C., USA. ILLUS. MAPS.
ISBN: 1-55581-005-5.
DT Book
FS BR
LA ENGLISH
ED Entered STN: 27 Jun 1989
Last Updated on STN: 27 Jun 1989
TI ANTIGENIC VARIATION IN RELAPSING FEVER ***BORRELIA*** SPECIES GENETICS ASPECTS.
IT Miscellaneous Descriptors
REVIEW OUTER MEMBRANE PROTEINS DNA REARRANGEMENT ***VMP*** GENES SWITCHING

L4 ANSWER 83 OF 87 LIFESCI COPYRIGHT 2009 CSA on STN
AN 89:7791 LIFESCI <<LOGINID::20090609>>
TI Antigenic variation in relapsing fever ***Borrelia*** species: Genetic aspects.
MOBILE DNA.
AU Barbour, A.; Berg, D.E. [editor]; Howe, M.M. [editor]
CS Dep. Microbiol., Univ. Texas Health Sci. Cent., 7703 Floyd Curl Dr., San Antonio, TX 78284-7758, USA
SO (1989) pp. 783-790.
ISBN: 1-55581-005-5.
DT Book
TC General Review
FS J; G
LA English

AB The following aspects are covered in this review: biology and immunology of relapsing fever ***borreliae*** ; outer membrane proteins are determinants of serotype specificity; antigenic variation is the consequence of DNA rearrangements; the ***vmp*** genes are on linear plasmids; and possible mechanisms of ***vmp*** gene switching.
TI Antigenic variation in relapsing fever ***Borrelia*** species: Genetic aspects.
MOBILE DNA.
AB The following aspects are covered in this review: biology and immunology of relapsing fever ***borreliae*** ; outer membrane proteins are determinants of serotype specificity; antigenic variation is the consequence of DNA rearrangements; the ***vmp*** genes are on linear plasmids; and possible mechanisms of ***vmp*** gene switching.
UT reviews; membrane proteins; genes; ***Borrelia*** ; antigenic variants; genetic variance; ***vmp*** gene

L4 ANSWER 84 OF 87 EMBASE COPYRIGHT (c) 2009 Elsevier B.V. All rights reserved on STN
AN 1988223362 EMBASE <<LOGINID::20090609>>
TI Genetic mechanisms of bacterial antigenic variation.
AU Seifert, H.S.; So, M.
CS Department of Microbiology and Immunology, Northwestern Medical and Dental Schools, Chicago, IL 60611, United States.
SO Microbiological Reviews, (1988) Vol. 52, No. 3, pp. 327-336.
ISSN: 0146-0749 CODEN: MBRED3
CY United States
DT Journal; General Review; (Review)
FS 026 Immunology, Serology and Transplantation
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
LA English
SL English
ED Entered STN: 11 Dec 1991
Last Updated on STN: 11 Dec 1991
AB The studies described above indicate that procaryotes have evolved a variety of mechanisms to vary their surface coats. N. gonorrhoeae primarily uses DNA transformation to effect pilus antigenic variation at the recombinational level. It also uses recombination (and perhaps also DNA transformation) to bring about P.II antigenic variation at the translational level. Finally, ***Borrelia*** organisms have evolved a plasmid recombination system to undergo ***VMP*** antigenic variation. To place procaryotic antigenic variation into proper perspective, we end this review with a brief consideration of the host immune system. Mammals have also evolved what could be considered an antigenic variation system, i.e., the generation of antibodies with different antigen-binding specificities. The arrangement of multiple copies of V, D, and J gene segments in the mammalian genome is reminiscent of the arrangement of silent pilin gene segments in the gonococcal chromosome. However, unlike pilin, P.II, and ***VMP*** expression, the generation of a functional expressing immunoglobulin gene does not involve expression sites. Instead, a complete immunoglobulin gene is created by recombinational joining of various gene segments, with concomitant deletion of intervening sequences. A system that appears to resemble the gonococcal pilin mechanism has been described for chicken immunoglobulin light chains. The light chain variants all are derived from a unique V-J rearrangement, with diversification occurring by gene conversion from other V gene copies to this single expressed gene within the Bursa of Fabricius. Four main processes appear to be responsible for the generation of antibody

diversity in mammalian cells. The first, known as 'combinational diversity', is the joining of V and J gene segments in various combinations. Diversity could also be generated by imprecise joining at V-J, V-D, and D-J junctions. In addition, joining of the V(H)-D and D-J(H) segments could lead to insertion of one to several nucleotides at these junctions. Finally, sequence changes could occur in immunoglobulin gene segments by somatic mutation. Whether these four processes also contribute to antigenic variation in procaryotic systems is not known at present. Since both the procaryotic and eucaryotic systems operate at the recombinational level, it is possible that the first three processes which contribute to immunoglobulin diversity also play a role in procaryotic antigenic variation. As for somatic mutations, it is clear that antigenic drift contributes significantly to the generation of hemagglutinin and neuraminidase variants of the flu virus. It is therefore likely that this process also contributes to sequence variability of the pilin, P.II, and ***VMP*** genes. In addition, gene conversion is thought to contribute to the generation of somatic mutation in immunoglobulin genes. In summary, it is interesting to note that the systems of antigenic variation and immunoglobulin diversification have evolved in a similar and complementary fashion, with DNA recombination playing a central mechanistic role. It is highly likely that the two systems developed together, with each providing the evolutionary pressure needed by the other. Finally, the examples of antigenic variation covered in this review illustrate the fascinating and diverse ways microbes have found to regulate and alter gene expression.

AB . . . It also uses recombination (and perhaps also DNA transformation) to bring about P.II antigenic variation at the translational level. Finally, ***Borrelia*** organisms have evolved a plasmid recombination system to undergo ***VMP*** antigenic variation. To place procaryotic antigenic variation into proper perspective, we end this review with a brief consideration of the. . . genome is reminiscent of the arrangement of silent pilin gene segments in the gonococcal chromosome. However, unlike pilin, P.II, and ***VMP*** expression, the generation of a functional expressing immunoglobulin gene does not involve expression sites. Instead, a complete immunoglobulin gene is. . . the flu virus. It is therefore likely that this process also contributes to sequence variability of the pilin, P.II, and ***VMP*** genes. In addition, gene conversion is thought to contribute to the generation of somatic mutation in immunoglobulin genes. In summary,. . .

L4 ANSWER 85 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 52

AN 1985:383147 BIOSIS <<LOGINID::20090609>>

DN PREV198580053139; BA80:53139

TI VARIABLE MAJOR PROTEINS OF ***BORRELIA*** -HERMSII EPITOPE MAPPING AND PARTIAL SEQUENCE ANALYSIS OF CYANOGEN BROMIDE PEPTIDES.

AU BARSTAD P A [Reprint author]; COLIGAN J E; RAUM M G; BARBOUR A G

CS LAB MICROBIAL STRUCTURE FUNCTION, ROCKY MOUNTAIN LAB, NATL INST ALLERGY INFECTIOUS DISEASES, HAMILTON, MONTANA 59840, USA

SO Journal of Experimental Medicine, (1985) Vol. 161, No. 6, pp. 1302-1314. CODEN: JEMEAV. ISSN: 0022-1007.

DT Article

FS BA

LA ENGLISH

AB The variable major proteins (***VMP***) of serotypes 7 and 21 of the relapsing fever agent B. hermsii were isolated by detergent extraction and high performance liquid chromatography. CNBr digestion of the isolated

VMP yielded 2 peptides of apparent MW 20,000 (20 K) and 16 K from ***VMP7*** , and 3 peptides of 14.5, 14, and 7 K MW from ***VMP21***

.

Serotype-specific monoclonal antibodies bound in Western blots to 1 of each of the 2 or 3 CNBr fragments from the homologous ***VMP*** . A single monoclonal antibody bound to the whole cells, the isolated ***VMP*** , and a CNBr fragment of both serotype 7 and serotype 21. (This cross-reactive antibody did not, however, bind to any of 4 other serotypes examined). Regional conservation of structure between ***VMP7*** and ***VMP21*** was also shown by amino acid sequence analysis of the N-termini of the 5 CNBr fragments. One pair of aligned fragments from ***VMP7*** and ***VMP21*** had 80% amino acid homologies between 2 ***VMP*** suggest that these proteins are products of members of a polygene family.

TI VARIABLE MAJOR PROTEINS OF ***BORRELIA*** -HERMSII EPITOPE MAPPING AND PARTIAL SEQUENCE ANALYSIS OF CYANOGEN BROMIDE PEPTIDES.

AB The variable major proteins (***VMP***) of serotypes 7 and 21 of the relapsing fever agent B. hermsii were isolated by detergent extraction and high performance liquid chromatography. CNBr digestion of the isolated ***VMP*** yielded 2 peptides of apparent MW 20,000 (20 K) and 16 K from ***VMP7*** , and 3 peptides of 14.5, 14, and 7 K MW from ***VMP21***

.

Serotype-specific monoclonal antibodies bound in Western blots to 1 of each of the 2 or 3 CNBr fragments from the homologous ***VMP*** . A single monoclonal antibody bound to the whole cells, the isolated ***VMP*** , and a CNBr fragment of both serotype 7 and serotype 21. (This cross-reactive antibody did not, however, bind to any of 4 other serotypes examined). Regional conservation of structure between ***VMP7*** and ***VMP21*** was also shown by amino acid sequence analysis of the N-termini of the 5 CNBr fragments. One pair of aligned fragments from ***VMP7*** and ***VMP21*** had 80% amino acid homologies between 2 ***VMP*** suggest that these proteins are products of members of a polygene family.

L4 ANSWER 86 OF 87 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 53

AN 1986:142045 BIOSIS <<LOGINID::20090609>>

DN PREV198681052461; BA81:52461

TI TRANSPOSITION OF STRUCTURAL GENES TO AN EXPRESSION SEQUENCE ON A LINEAR PLASMID CAUSES ANTIGENIC VARIATION IN THE BACTERIUM ***BORRELIA*** -HERMSII.

AU PLASTERK R H A [Reprint author]; SIMON M I; BARBOUR A G

CS CALIFORNIA INST TECHNOLOGY, DIV BIOLOGY 147-75 PASADENA, CALIFORNIA 91125, USA

SO Nature (London), (1985) Vol. 318, No. 6043, pp. 257-263.
CODEN: NATUAS. ISSN: 0028-0836.

DT Article

FS BA

LA ENGLISH

ED Entered STN: 25 Apr 1986
Last Updated on STN: 25 Apr 1986

AB In ***Borrelia*** hermsii, a spirochaete that causes relapsing fever, the switch between expression of two frequent variable major protein (***VMP***) types (7 and 21) is associated with a DNA rearrangement. Both cell types 7 and 21 contain untranscribed 7 and 21 ***VMP***

genes on linear plasmids. The serotype 7 cells contain an additional copy of the 7 ***VMP*** gene fused to an expression sequence on another linear plasmid. Switching to the 21 serotype involves removal of the transcribed 7 ***VMP*** gene and fusion of a copy of the 21 ***VMP*** gene to this same expression sequence. Thus, recombination between linear plasmids can activate different ***VMP*** genes.

TI TRANSPOSITION OF STRUCTURAL GENES TO AN EXPRESSION SEQUENCE ON A LINEAR PLASMID CAUSES ANTIGENIC VARIATION IN THE BACTERIUM ***BORRELIA*** -HERMSII.

AB In ***Borrelia*** hermsii, a spirochaete that causes relapsing fever, the switch between expression of two frequent variable major protein (***VMP***) types (7 and 21) is associated with a DNA rearrangement. Both cell types 7 and 21 contain untranscribed 7 and 21 ***VMP*** genes on linear plasmids. The serotype 7 cells contain an additional copy of the 7 ***VMP*** gene fused to an expression sequence on another linear plasmid. Switching to the 21 serotype involves removal of the transcribed 7 ***VMP*** gene and fusion of a copy of the 21 ***VMP*** gene to this same expression sequence. Thus, recombination between linear plasmids can activate different ***VMP*** genes.

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AN 1986060790 EMBASE <<LOGINID::20090609>>

TI Transposition of structural genes to an expression sequence on a linear plasmid causes antigenic variation in the bacterium ***Borrelia*** hermsii.

AU Plasterk, R.H.A.; Simon, M.I.; Barbour, A.G.

CS California Institute of Technology, Division of Biology 147-75, Pasadena, CA 91125, United States.

SO Nature, (1985) Vol. 31 B, No. 6043, pp. 257-263.
ISSN: 0028-0836 CODEN: NATUAS

CY United Kingdom

DT Journal

FS 022 Human Genetics
026 Immunology, Serology and Transplantation
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology

LA English

ED Entered STN: 10 Dec 1991
Last Updated on STN: 10 Dec 1991

AB In ***Borrelia*** hermsii, a spirochaete that causes relapsing fever, the switch between expression of two frequent variable major protein (***VMP***) types (7 and 21) is associated with a DNA rearrangement. Both cell types 7 and 21 contain untranscribed 7 and 21 ***VMP*** genes on linear plasmids. The serotype 7 cells contain an additional copy of the 7 ***VMP*** gene fused to an expression sequence on another linear plasmid. Switching to the 21 serotype involves removal of the transcribed 7 ***VMP*** gene and fusion of a copy of the 21 ***VMP*** gene to this same expression sequence. Thus recombination between linear plasmids can activate different ***VMP*** genes.

TI Transposition of structural genes to an expression sequence on a linear plasmid causes antigenic variation in the bacterium ***Borrelia*** hermsii.

AB In ***Borrelia*** hermsii, a spirochaete that causes relapsing fever, the switch between expression of two frequent variable major protein (***VMP***) types (7 and 21) is associated with a DNA rearrangement. Both cell types 7 and 21 contain untranscribed 7 and 21 ***VMP*** genes on linear plasmids. The serotype 7 cells contain an additional copy

of the 7 ***VMP*** gene fused to an expression sequence on another linear plasmid. Switching to the 21 serotype involves removal of the transcribed 7 ***VMP*** gene and fusion of a copy of the 21 ***VMP*** gene to this same expression sequence. Thus recombination between linear plasmids can activate different ***VMP*** genes.

CT Medical Descriptors:
****borrelia hermsii***
gene translocation
heredity
nonhuman
*plasmid
priority journal
*serotype
*antigen
*bacterial antigen

An alternative to view hit terms when display exceeds KWIC processing limits is to use HIT display format.